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(54) Title: cDNA ENCODING A TRAG GENE (TGF- β RESISTANCE ASSOCIATED GENE) AND ITS PROTEIN PRODUCT

(57) Abstract: Nucleic acids that encode novel polypeptides, designated in the present application as "TRAG" (TGF- β Resistance Associated Gene) are provided. TRAG is overexpressed in a number of transformed rat liver epithelial (RLE) cell lines resistant to the growth inhibitory effect of TGF- β 1 as well as in primary liver tumors. Compositions including TRAG chimeras, nucleic acids encoding TRAG, and antibodies to TRAG are also provided. Methods of using TRAG to screen for cancer cells, to screen for aggressive metastasis in cells, to screen for targets for cancer therapy, and to study cell proliferation are further provided.

cDNA ENCODING A TRAG GENE (TGF- β RESISTANCE ASSOCIATED GENE)
AND ITS PROTEIN PRODUCT

This application is being filed as a PCT International Patent application on
5 February 12, 2001, designating all countries, in the name of The Government of the
United States, represented by the Secretary, Department of Health and Human Services
(applicant for all countries except the U.S.), and in the names of Snorri S. Thorgeirsson,
a U.S. citizen, and Sean Sanders, a South African citizen (applicants for U.S. only).

10 FIELD OF THE INVENTION

The present invention relates generally to the isolation and characterization of
novel DNA and polypeptides, designated herein as "TRAG."

BACKGROUND OF THE INVENTION

15 The ligand transforming growth factor-beta (TGF- β) has a wide range of
physiological and pathological effects in epithelial cells (which includes liver cells),
including inhibition of cell proliferation, stimulation of cell differentiation, matrix
production, and apoptosis. (J. Massagué, Annual Rev. Cell Biol., 6:597 (1990)). TGF- β
can suppress uncontrolled cell proliferation and induce cell death (apoptosis) in
20 damaged/redundant cells by signaling through membrane receptors (TGF- β receptor type
I, T β RI; TGF- β receptor type II, T β RII) and intracellular signal transduction proteins
(for example, SMAD2, SMAD3, and SMAD4). (M. Kawabata et al., J. Biochem., 125:9
(1999)). More importantly, many tumor types, and particularly those in the liver, have
been shown to lose sensitivity to TGF- β . That is, these cells are not susceptible to
25 abrogation of cell division or death induced by TGF- β . This can occur in a number of
different ways, including through loss of one of the two TGF- β receptors or through
disruption of the intracellular signaling pathway (such as loss of mutation of one of the
SMAD proteins). (See, for example, K.R. Cho et al., J. Biol. Chem. Suppl., 137 (1992)
and A. Kiss et al., Clin. Cancer Res., 3:1059 (1997)).

30 Recently, a number of new proteins that interact with one or more components of
the TGF- β signaling pathway have been discovered. These include TRIP-1, which has
been shown to associate with, and be biochemically modified by, T β RII, and STRAP,
which can interact with both T β RI and T β RII. (R.H. Chen et al., Nature, 377:548 (1995))

and P.K. Datta et al., J. Biol. Chem., 273(52):34671 (1998)). Both of these proteins contain conserved domains known as WD repeats. These repeats are ~40 amino acids in length and follow a loosely conserved consensus sequence. (E.J. Neer et al., Nature, 371:297 (1994)). WD repeat-containing proteins are believed to interact through these conserved domains and are involved in a plethora of cellular and molecular pathways including signal transduction, gene regulation, protein trafficking, and RNA processing. (E.J. Neer et al., Nature, 371:297 (1994)).

It is desirable to identify and characterize new cellular genes encoding proteins involved in TGF- β signaling. The identification and characterization of new genes encoding proteins involved in TGF- β signaling are particularly useful for better understanding TGF- β signaling pathways such as, for example, useful for studying mechanisms of cell proliferation and the means to modulate such activity, and particularly useful for screening targets for cancer therapy.

SUMMARY OF THE INVENTION

Applicants have identified nucleotide sequences that encode a novel polypeptide, designated in the present application as "TRAG" (TGF- β Resistance Associated Gene), which exhibits a number of characteristics that make it a useful tool for studying cell-cycle control and oncogenesis. TRAG is a previously undescribed gene. TRAG has multiple WD repeat elements and two tyrosine phosphorylation motifs. WD repeat elements are known to be involved in protein-protein interactions, which control many aspects of cell growth, differentiation, and survival. Tyrosine phosphorylation motifs can play a role in the modulation of protein function. As such, this novel protein has a variety of applications in the identification, characterization, and regulation of activities associated with cellular regulation as well as processes associated with oncogenesis. It is believed that TRAG plays an important role in TGF- β signal transduction, normal cell function, and organogenesis.

In one embodiment, the invention provides an isolated nucleic acid molecule that includes nucleotides that encode a TRAG polypeptide. For example, the isolated nucleic acid can include DNA encoding a TRAG polypeptide having amino acid residues 1 to 1488 of Table 1, amino acid residues 1 to 1490 of Table 2, or amino acid residues 1 to 1489 of Table 3 or can include DNA complementary to such an encoding nucleic acid sequence of Table 1, 2, or 3, which remains stably bound to it under at least moderate,

and optionally, under high stringency conditions. In another embodiment, the invention provides a vector comprising a gene encoding a TRAG polypeptide. A host cell comprising such a vector is also provided. By way of example, the host cells may be *E. coli*, yeast, insect, fungal, or mammalian cells. A process for producing TRAG
5 polypeptides is further provided and comprises culturing host cells under conditions suitable for expression of TRAG. If desired, the TRAG polypeptide can be recovered.

In one embodiment, the invention provides an isolated polypeptide comprising a TRAG fragment, wherein the TRAG fragment comprises multiple WD repeat elements and two tyrosine phosphorylation motifs. In a favored embodiment, the isolated
10 polypeptide exhibits TRAG-like activity and, typically, is capable of interacting with other WD repeat element-containing proteins. In another embodiment, the invention provides isolated TRAG polypeptide. In particular, the invention provides isolated native sequence TRAG polypeptide, which in one embodiment, includes an amino acid sequence comprising residues 1 to 1488 of Table 1, an amino acid sequence comprising
15 residues 1 to 1490 of Table 2, or an amino acid sequence comprising residues 1 to 1489 of Table 3. In a related embodiment, the invention provides chimeric molecules comprising TRAG polypeptide fused to a heterologous polypeptide or amino acid sequence. An example of such a chimeric molecule is a factor that includes a TRAG fused to a protein such as the maltose-binding protein. In yet another embodiment, the
20 invention provides a polypeptide capable of specifically binding a TRAG polypeptide such as an antibody specific for a TRAG polypeptide.

In other embodiments, the invention provides methods for using TRAG-RELATED polypeptides and nucleic acids for studying and modulating mechanisms involved in cellular proliferation. In one embodiment, the invention provides a method
25 of modulating cellular phenotype by controlling the level of TRAG expression within the cell. For example, mammalian cells can be transfected with a DNA vector encoding a TRAG polypeptide having the amino acid sequence of Table 1, 2, or 3. The TRAG polypeptide can be expressed in the cells, and cells having an altered phenotype such as, for example, cancer cells or cells having aggressive metastasis, can then be selected.

30 Alternatively, the invention provides a method of reducing TRAG expression via antisense oligonucleotides to effect a cellular phenotype such as TGF- β sensitivity. In a related embodiment, the invention provides methods for effecting the interaction between TRAG and other WD repeat element-containing proteins.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1A shows the normal expression pattern of TRAG in various rat tissues according to a Northern blot analysis. This Northern blot shows mRNA (total and poly-
5 A⁺) extracted from 3 rat cell lines (RLE, B5T, and C4T).

Figure 1B shows a graphical representation of the data from Figure 1A after the levels of TRAG mRNA were quantified. Data was quantified using a densitometric scan of the phosphoimager plate (to which the radioactive membrane was exposed) by making use of ImageQuant[™] Version 3.3 software (Molecular Dynamics).

10 Figure 2A shows the genetic localization of the TRAG gene to chromosome 18 in mouse (region is 18D.1-E.3). This localization was determined by using a DNA probe complementary to a portion of the TRAG gene, covering exons 14 to 21 (left panel). The right panel shows a similar experiment, but performed using a DNA probe that reacts exclusively with the entire mouse chromosome 18.

15 Figure 2B shows the genetic localization of the TRAG gene to chromosome 18 in human (region is 18q 21.1-22). This localization was determined by using a ~5kb DNA probe against a centrally located region of the TRAG gene spanning exons 12 to 14 (left panel). The right panel shows a similar experiment, but performed using a DNA probe that reacts exclusively with the entire human chromosome 18.

20 Figure 3A shows the size and qualitative levels of TRAG mRNA expressed in normal rat tissue from heart, brain, spleen, lung, liver, muscle, kidney, and testis. mRNA transcripts having sizes of approximately 7.2 kb and 3.5 kb were identified. The brain tissue shows a smear of multiple mRNAs, which can be the result of alternative splicing of a single mRNA transcript.

25 Figure 3B shows a dot blot hybridization using a commercial membrane containing rat mRNA from brain, heart, gastrointestinal tract (GIT), numerous internal organs including liver and testis (indicated), tumor cell lines (labeled "lines"), and fetal tissue (from top: brain, heart, kidney, liver, spleen, thymus, and lung). TRAG mRNA was expressed in all tissues but appeared to be most abundant in brain.

30 Figure 3C shows a dot blot hybridization using a commercial membrane containing mouse mRNA from (top, L to R) brain, eye, liver, lung, kidney, heart, skeletal muscle, smooth muscle, pancreas, thyroid, thymus, submaxillary gland, spleen, testis, ovary, prostate, epididymus, uterus, and embryo (7 days, 11 days, 15 days, and 17 days). TRAG expression was identified in all tissues.

Figure 4 shows a Western blot of TRAG protein extracted from three rat cell lines (B5T, C4T, and RLE phi 13). This blot shows elevated levels of TRAG protein in transformed B5T and C4T cells relative to untransformed RLE cells.

Figure 5A shows a Western blot of TRAG protein extracted from chemically transformed rat cell lines (AFL-B8 and AFL-D8) and virally transformed rat cell lines (3611T2, 3611T5, and J2-14). This blot also includes samples from RLE and B5T cells as negative and positive controls, respectively. A Northern blot, which shows the expression of TRAG mRNA in these cell lines, is also shown.

Figure 5B shows a Western blot of TRAG protein extracted from tumor cell lines derived from double transgenic *c-myc/TGF- α* mice. A Northern blot, which shows the TRAG mRNA levels in these cell lines, is also shown.

Figure 5C shows a Western blot of TRAG protein extracted from Alex, Chang, FOCUS, HepG2, Huh-7, Sk-Hep-1, WRL-68, and HeLa human tumor cell lines. A Northern blot, which shows the TRAG mRNA levels in these cell lines, is also shown.

Figure 5D shows a Western blot of TRAG protein extracted from primary tumors taken from double transgenic *c-myc/TGF- α* mice. This blot also includes samples from RLE and B5T cells as negative and positive controls, respectively.

Figure 6A shows confocal microscope images of RLE and B5T cells transfected with either a control green fluorescent protein (GFP only) plasmid or with a vector containing the TRAG gene fused to the green fluorescent protein (TRAG-GFP). The images show that the TRAG protein is localized to the cytoplasm of both RLE and B5T cells.

Figure 6B shows an immunohistochemical stain of paraformaldehyde-fixed RLE and B5T cells. The TRAG protein was stained by using an anti-TRAG polyclonal antibody. The stain shows that the TRAG protein is localized to the cytoplasm of both RLE and B5T cells and appears to be perinuclear.

DETAILED DESCRIPTION OF THE INVENTION

I. Definitions

The terms "TRAG polypeptide" and "TRAG" when used herein encompass native sequence TRAG and TRAG variants (which are further defined herein). TRAG may be isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant or synthetic methods.

The TRAG polypeptide, which may be a fragment of a native sequence, contains multiple WD repeat elements and 2 tyrosine phosphorylation motifs.

A "native sequence TRAG" is a polypeptide having the same amino acid sequence as TRAG derived from nature. Such native sequence TRAG can be isolated from nature or can be produced by recombinant or synthetic means. The term "native sequence TRAG" specifically encompasses naturally-occurring variant forms (e.g., alternatively spliced forms) and naturally-occurring allelic variants of the TRAG. In one embodiment of the invention, the native sequence TRAG is a mature or full-length native sequence TRAG polypeptide comprising amino acids 1 to 1488 of Table 1. Alternately, the TRAG polypeptide comprises amino acid residues 1 to 1490 of Table 2 or amino acid residues 1 to 1489 of Table 3.

"TRAG variant" means a functionally active TRAG as defined below having at least about 80% amino acid sequence identity with TRAG, such as the TRAG polypeptide having the deduced amino acid sequence shown in Tables 1, 2, or 3 for a full-length native sequence TRAG. Such TRAG variants include, for instance, TRAG polypeptides wherein one or more amino acid residues are added to or deleted from the N-terminus or C-terminus of the sequence of Tables 1, 2, or 3. Ordinarily, a TRAG variant will have at least about 80% or 85% amino acid sequence identity with native TRAG sequences, more preferably at least about 90% amino acid sequence identity. Even more preferably a TRAG variant will have at least about 95% amino acid sequence identity with the native TRAG sequence of Tables 1, 2, or 3. As noted above, TRAG variants include multiple WD repeat elements and 2 tyrosine phosphorylation motifs. Functionally active TRAG variants typically have at least about 50 amino acid residues and preferably at least about 100 amino acid residues.

"Percent (%) amino acid sequence identity" with respect to the TRAG sequences identified herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the TRAG sequence after aligning the sequences in the same reading frame and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full

length of the sequence being compared.

"Percent (%) nucleic acid sequence identity" with respect to the TRAG sequences identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the TRAG sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared.

The term "epitope tagged" when used herein refers to a chimeric polypeptide comprising TRAG, or a functional fragment thereof, fused to a "tag polypeptide." The tag polypeptide has enough residues to provide an epitope against which an antibody can be made, or which can be identified by some other agent, yet is short enough that it does not interfere with the activity of TRAG. The tag polypeptide preferably also is sufficiently unique so that the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 and about 50 amino acid residues (preferably, between about 10 and about 20 residues).

"Isolated," when used to describe the various polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the polypeptide will be purified to a degree sufficient to obtain N-terminal or internal amino acid sequence by use of a spinning cup sequenator or to homogeneity by SDS-PAGE under nonreducing or reducing conditions using Coomassie blue or silver stain. Isolated polypeptide includes polypeptide *in situ* within recombinant cells because at least one component of the TRAG natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step (referred to herein as an "isolated and purified polypeptide").

An "isolated" TRAG nucleic acid molecule is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which

is ordinarily associated in the natural source of the TRAG nucleic acid. An isolated TRAG nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated TRAG nucleic acid molecules therefore are distinguished from the TRAG nucleic acid molecule as it exists in natural cells. However, an isolated TRAG nucleic acid molecule includes TRAG nucleic acid molecules contained in cells that
5 ordinarily express TRAG where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The
10 control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory
15 leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are
20 contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking may be accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers may be used in accordance with conventional practice.

25 "Polynucleotide" and "nucleic acid" refer to single- or double-stranded molecules, which may be DNA, comprised of the nucleotide bases A, T, C and G, or RNA, comprised of the bases A, U (substitutes for T), C, and G. The polynucleotide may represent a coding strand or its complement. Polynucleotide molecules may be identical in sequence to the sequence that is naturally occurring or may include alternative codons
30 that encode the same amino acid as that which is found in the naturally occurring sequence (*See* Lewin, Genes V, Oxford University Press, Chapter 7, pp. 171-174 (1994)). Furthermore, polynucleotide molecules may include codons that represent

conservative substitutions of amino acids as described. The polynucleotide may represent genomic DNA or cDNA.

"Polypeptide" refers to a molecule comprised of amino acids that correspond to those encoded by a polynucleotide sequence that is naturally occurring. The polypeptide
5 may include conservative substitutions where the naturally occurring amino acid is replaced by one having similar properties, where such conservative substitutions do not alter the function of the polypeptide (*See* Lewin, Genes V, Oxford University Press, Chapter 1, pp. 9-13 (1994)).

The term "antibody" is used in the broadest sense and specifically covers single
10 anti-TRAG monoclonal antibodies (including agonist, antagonist, and neutralizing antibodies) and anti-TRAG antibody compositions with polypepitopic specificity. The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, *i.e.*, the individual antibodies comprising the population are identical except for possible naturally-occurring mutations
15 that may be present in minor amounts.

The term "mammal" as used herein refers to any mammal classified as a mammal, including humans, cows, horses, dogs, and cats. In a preferred embodiment of the invention, the mammal is a human.

20 II. Compositions and Methods of the Invention

A. TRAG Nucleic Acids and Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as TRAG. In particular, Applicants have identified and isolated genes and cDNA encoding TRAG
25 polypeptides, as disclosed in further detail in the Examples below. Using sequence homology searches, Applicants found that TRAG (as shown in Tables 1, 2, and 3) contains multiple WD repeat elements, which are found in other proteins such as TRIP-1 and STRAP, known to interact with proteins in the TGF- β signaling pathway. Two tyrosine phosphorylation motifs were also identified. These motifs can play a role in the
30 modulation of protein function through addition or removal of phosphate molecules at the tyrosine residue.

In addition to the full-length native sequence TRAG and soluble forms of TRAG

described herein, it is contemplated that TRAG variants can be prepared. TRAG variants can be prepared by introducing appropriate nucleotide changes into the TRAG nucleotide sequence, or by synthesis of the desired TRAG polypeptide. Those skilled in the art will appreciate that amino acid changes may alter post-translational processes of the TRAG, such as changing the number or position of glycosylation sites or altering the protein binding characteristics. Variations in the native full-length sequence TRAG or in various domains of the TRAG described herein, can be made, for example, using any of the techniques and guidelines for conservative and nonconservative mutations set forth, for instance, in U.S. Patent No. 5,364,934. For example, amino acid substitutions within the tyrosine phosphorylation motifs are contemplated, such as conservative substitutions at one or both of these residues.

Variations may be a substitution, deletion, or insertion of one or more codons encoding the TRAG that results in a change in the amino acid sequence of the TRAG as compared with the native sequence TRAG. Optionally the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of the TRAG. Guidance in determining which amino acid residue may be inserted, substituted, or deleted without adversely affecting the desired activity may be found by comparing the sequence of the TRAG with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, i.e., conservative amino acid replacements. Insertions or deletions may optionally be in the range of 1 to 5 amino acids. The variation allowed may be determined by systematically making insertions, deletions or substitutions of amino acids in the sequence and testing the resulting variants for activity in any of the *in vitro* assays described in the Examples below.

It is a well-established principle of protein chemistry that certain amino acid substitutions, entitled "conservative amino acid substitutions," can frequently be made in a protein without altering either the conformation or the function of the protein. Such changes include substituting any of isoleucine (I), valine (V), and leucine (L) for any other of these hydrophobic amino acids; aspartic acid (D) for glutamic acid (E) and vice versa; glutamine (Q) for asparagine (N) and vice versa; and serine (S) for threonine (T) and vice versa. Other substitutions can also be considered conservative, depending on the environment of the particular amino acid and its role in the three-dimensional structure of

the protein. For example, glycine (G) and alanine (A) can frequently be interchangeable, as can alanine and valine (V).

Methionine (M), which is relatively hydrophobic, can frequently be interchanged with leucine and isoleucine, and sometimes with valine. Lysine (K) and arginine (R) are frequently interchangeable in locations in which the significant feature of the amino acid residue is its charge and the differing pK's of these two amino acid residues are not significant. Still other changes can be considered "conservative" in particular environments.

Variations can be made using methods known in the art such as site-directed mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis (Carter et al., Nucl. Acids Res., 13:4331 (1986); Zoller et al., Nucl. Acids Res., 10:6487 (1987)), cassette (Wells et al., Gene, 34:315 (1985)), restriction selection mutagenesis (Wells et al., Philos. Trans. R. Soc. London SerA, 317:415 (1986)) or other known techniques can be performed on the cloned DNA to produce the TRAG variant DNA. Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions (Creighton, The Proteins (W.H. Freeman & Co., N.Y.); Chothia, J. Mol. Biol., 150:1 (1976)). If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

As discussed above, redundancy in the genetic code permits variation in TRAG gene sequences. In particular, one skilled in the art will recognize specific codon preferences by a specific host species and can adapt the disclosed sequence as preferred for a desired host. For example, preferred codon sequences typically have rare codons (i.e., codons having a usage frequency of less than about 20% in known sequences of the desired host) replaced with higher frequency codons. Codon preferences for a specific organism may be calculated, for example, by utilizing codon usage tables available on the INTERNET at the following address:
<http://www.dna.affrc.go.jp/~nakamura/codon.html>. Nucleotide sequences that have been optimized for a particular host species by replacing any codons having a usage

frequency of less than about 20% are referred to herein as "codon optimized sequences."

Additional sequence modifications are known to enhance protein expression in a cellular host. These include elimination of sequences encoding spurious polyadenylation signals, exon/intron splice site signals, transposon-like repeats, and/or other such well-
5 characterized sequences that may be deleterious to gene expression. The GC content of the sequence may be adjusted to levels average for a given cellular host, as calculated by reference to known genes expressed in the host cell. Where possible, the sequence may also be modified to avoid predicted hairpin secondary mRNA structures. Other useful
10 modifications include the addition of a translational initiation consensus sequence at the start of the open reading frame, as described in Kozak, Mol. Cell Biol., 9:5073-5080 (1989). Nucleotide sequences that have been optimized for expression in a given host species by elimination of spurious polyadenylation sequences, elimination of exon/intron splicing signals, elimination of transposon-like repeats, and/or optimization of GC
15 content in addition to codon optimization are referred to herein as an "expression enhanced sequence."

B. Modifications of TRAG

Covalent modifications of TRAG are included within the scope of this invention.
20 One type of covalent modification includes reacting targeted amino acid residues of the TRAG with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C- terminal residues of the TRAG. Derivatization with bifunctional agents is useful, for instance, for crosslinking TRAG to a water-insoluble support matrix or surface for use in the method for purifying anti-TRAG antibodies, and vice-versa.
25 Commonly used crosslinking agents include, *e.g.*, 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimidate. In the
30 alternative, TRAG can be joined to a detectable label such as a radioactive isotope such as I^{125} or P^{32} , an enzyme such as horseradish peroxidase or alkaline phosphatase, a fluorophore such as fluorescein isothiocyanate or a chromophore (Current Protocols In Molecular Biology, Volume 2, Units 10, 11 and 14, Frederick M. Ausubul et al. eds., 1995; Molecular Cloning. A Laboratory Manual, § 12, Tom Maniatis et al. eds., 2d ed.

1989).

Another type of covalent modification of the TRAG polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence TRAG, and/or adding one or more glycosylation sites that are not present in the native sequence TRAG. Addition of glycosylation sites to the TRAG polypeptide may be accomplished by altering the amino acid sequence. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence TRAG (for O-linked glycosylation sites). The TRAG amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the TRAG polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids. Another means of increasing the number of carbohydrate moieties on the TRAG polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, CRC Crit. Rev. Biochem., pp. 259-306 (1981).

The TRAG of the present invention may also be modified in a way to form a chimeric molecule comprising TRAG fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of the TRAG with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl- terminus of the TRAG. The presence of such epitope-tagged forms of the TRAG can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the TRAG to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag.

In an alternative embodiment, the chimeric molecule may comprise a fusion of the TRAG with an immunoglobulin or a particular region of an immunoglobulin. The TRAG may be fused to any one of a variety of known fusion protein partners that are well known in the art such as maltose binding protein, *LacZ*, thioredoxin, or an immunoglobulin constant region (Current Protocols In Molecular Biology, Volume 2, Unit 16, Frederick M. Ausubul et al. eds., 1995; Linsley et al., J.Exp. Med., 174:561-566 (1991)). In a preferred embodiment, this fusion partner is a non-TRAG binding molecule

so as to prevent difficulties associated with intramolecular interactions. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule. Other fusion proteins and tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 (Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7, and 9E10 antibodies thereto (Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky et al., Protein Engineering, 3(6):547-553 (1990)). Other tag polypeptides include the Flag-peptide (Hopp et al., BioTechnology, 6:1204-1210 (1988)); the KT3 epitope peptide (Martin et al., Science, 255:192-194 (1992)); an I-tubulin epitope peptide (Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)).

15

C. Preparation of TRAG

The description below relates primarily to production of TRAG by culturing cells transformed or transfected with a vector containing TRAG nucleic acid. It is, of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare TRAG. For instance, the TRAG sequence, or portions thereof, may be produced by direct peptide synthesis using solid-phase techniques (*see, e.g.*, Stewart et al., Solid-Phase Peptide Synthesis, W.H. Freeman Co., San Francisco, CA (1969); Merrifield, J. Am. Chem. Soc., 85:2149-2154 (1963)). *In vitro* protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be accomplished, for instance, using an Applied Biosystems Peptide Synthesizer (Foster City, CA) using manufacturer's instructions. Various portions of the TRAG may be chemically synthesized separately and combined using chemical or enzymatic methods to produce the full-length TRAG.

30 1. Isolation of DNA Encoding TRAG

Due to the large size of TRAG mRNA, and therefore cDNA, both the rat and mouse TRAG genes (coding regions only) were isolated using the RT-PCR and RACE-PCR techniques, as is well-known in the art. Primer oligonucleotides were synthesized (Gibco, BRL Life Technologies) and used to amplify cDNA (produced directly from rat

or mouse mRNA), as described in Example 1. Three portions of the mouse TRAG gene so amplified were joined through the use of restriction digestion and subcloning, as described in Example 8, to yield a full length gene of 4,467 nucleotides of coding sequence.

5 Alternately, DNA encoding TRAG may also be obtained from a cDNA library prepared from tissue expressing a TRAG mRNA. Accordingly, human TRAG DNA can be conveniently obtained from a cDNA library prepared from human tissue. The TRAG-encoding gene may also be obtained from a genomic library or by
10 oligonucleotide synthesis. Libraries can be screened with probes (such as antibodies to the TRAG or oligonucleotides of at least about 20-80 bases) designed to identify the gene of interest or the protein encoded by it. Illustrative libraries include mouse kidney cDNA library (mouse kidney 5'-stretch cDNA, Clontech laboratories, Inc.) and human
liver cDNA library (human liver 5' stretch plus cDNA, Clontech Laboratories, Inc.). Screening the cDNA or genomic library with the selected probe may be conducted using
15 standard procedures, such as described in Sambrook et al., Molecular Cloning: A Laboratory Manual (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding TRAG is to use PCR methodology (Sambrook et al., supra; Dieffenbach et al., PCR Primer: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 1995)).

20 For cDNA library screening, oligonucleotide sequences selected as probes should be of sufficient length and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art and include the use of radiolabels like ^{32}P -labeled ATP, biotinylation, or enzyme labeling.
25 Hybridization conditions, including moderate stringency and high stringency, are provided in Sambrook et al., supra.

Sequences identified in such library screening methods can be compared and aligned to other known sequences deposited and available in public databases such as GenBank or other private sequence databases. Sequence identity (at either the amino
30 acid or nucleotide level) within defined regions of the molecule or across the full-length sequence can be determined through sequence alignment using computer software programs which employ various algorithms to measure homology.

Nucleic acid having protein coding sequence may be obtained by screening selected cDNA or genomic libraries using the deduced amino acid sequence disclosed

herein for the first time, and, if necessary, using conventional primer extension procedures as described in Sambrook et al., supra, to detect precursors and processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

5 2. Selection and Transformation of Host Cells

Host cells are transfected or transformed with expression or cloning vectors described herein for TRAG production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as media,
10 temperature, pH, and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in Mammalian Cell Biotechnology: a Practical Approach M. Butler, ed. (IRL Press, 1991) and Sambrook et al., supra.

15 Methods of transfection are known to the ordinarily skilled artisan, for example by using lipofectin, CaPO₄, or electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook et al., supra, or electroporation is generally used for prokaryotes or other cells that contain substantial
20 cell-wall barriers. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., Gene, 23:315 (1983) and WO 89/05859 published 29 June 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, Virology, 52:456-457 (1978) can be employed. General aspects of mammalian cell host system
25 transformations have been described in U.S. Patent No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen et al., J. Bact., 130:946 (1977) and Hsiao et al., Proc. Natl. Acad. Sci. (USA), 76:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or
30 polycations, e.g., polybrene, polyornithine, may also be used. For various techniques for transforming mammalian cells, see Keown et al., Methods in Enzymology, 185:527-537 (1990) and Mansour et al., Nature, 336:348-352 (1988).

Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include but are

not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5 772 (ATCC 53,635)

- 5 Suitable host cells for the expression of glycosylated TRAG are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as *Drosophila* S2 and *Spodoptera* Sf9 cells. See e.g. Current Protocols In Molecular Biology, Volume I, Unit 16, Frederick M. Ausubul et al. eds., 1995. Examples of useful mammalian host cell lines include rat liver epithelial cells, Hugget, A. C. et. al, supra,
10 Chinese hamster ovary (CHO) and COS cells. More specific examples include monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., J. Gen Virol., 36:59 (1977)); Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, Proc. Natl. Acad. Sci. USA, 77:4216 (1980)); mouse sertoli cells (TM4, Mather,
15 Biol. Reprod., 23:243-251 (1980)); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); and mouse mammary tumor (MMT 060562, ATCC CCL51). The selection of the appropriate host cell is deemed to be within the skill in the art.

20 3. Selection and Use of a Replicable Vector

- The nucleic acid (e.g., cDNA or genomic DNA) encoding TRAG may be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence may be
25 inserted into the vector by a variety of procedures. In general, DNA is inserted into an appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription
30 termination sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques that are known to the skilled artisan.

TRAG may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which may be a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or

polypeptide. In general, the signal sequence may be a component of the vector, or it may be a part of the TRAG DNA that is inserted into the vector. The signal sequence may be a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, lpp, or heat-stable enterotoxin II leaders. For yeast secretion
5 the signal sequence may be, *e.g.*, the yeast invertase leader, alpha factor leader (including *Saccharomyces* and *Kluyveromyces* α -factor leaders, the latter described in U.S. Patent No. 5,010,182), or acid phosphatase leader, the *C. albicans* glucoamylase leader (EP 362,179 published 4 April 1990), or the signal described in WO 90/13646 published 15 November 1990. In mammalian cell expression, mammalian signal sequences may be
10 used to direct secretion of the protein, such as signal sequences from secreted polypeptides of the same or related species, as well as viral secretory leaders.

Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid
15 pBR322 is suitable for most Gram-negative bacteria, the P2 plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells.

Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer
20 resistance to antibiotics or other toxins, *e.g.*, ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, *e.g.*, the gene encoding D-alanine racemase for *Bacilli*.

An example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the TRAG nucleic acid, such as
25 Neomycin, DHFR, or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub et al., Proc. Natl. Acad. Sci. USA, 77:4216 (1980). A suitable selection gene for use in yeast is the *trp1* gene present in the yeast plasmid YRp7 (Stinchcomb et al., Nature, 282:39 (1979); Kingsman et al., Gene, 7:141 (1979);
30 Tschemper et al., Gene, 10:157 (1980)). The *trp1* gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 (Jones, Genetics, 85:12 (1977)).

Expression and cloning vectors usually contain a promoter operably linked to the TRAG nucleic acid sequence to direct mRNA synthesis. Promoters recognized by a

variety of potential host cells are well known. Promoters suitable for use with prokaryotic hosts include the β -lactamase and lactose promoter systems (Chang et al., Nature, 275:615 (1978); Goeddel et al., Nature, 281:544 (1979)), alkaline phosphatase, a tryptophan (trp) promoter system (Goeddel, Nucleic Acids Res., 8:4057 (1980); EP 5 36,776), and hybrid promoters such as the tac promoter (deBoer et al., Proc. Natl. Acad. Sci. USA, 80:21-25 (1983)). Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding TRAG.

Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase (Hitzeman et al., J. Biol. Chem., 255:2073 10 (1980)) or other glycolytic enzymes (Hess et al., J. Adv. Enzyme Reg., 7:149 (1968); Holland, Biochemistry, 17:4900 (1978)), such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

15 Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable 20 vectors and promoters for use in yeast expression are further described in EP 73,657.

TRAG transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis- 25 B virus, and Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter, and from heat-shock promoters, provided such promoters are compatible with the host cell systems.

Transcription of a DNA encoding TRAG by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of 30 DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, I-fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter

enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at a position 5' or 3' to the TRAG coding sequence but is preferably located at a site 5' from the promoter.

Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant,
5 animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the
10 mRNA encoding TRAG. Still other methods, vectors, and host cells suitable for adaptation to the synthesis of TRAG in recombinant vertebrate cell culture are described in Gething et al., Nature 293:620-625 (1981); Mantei et al., Nature 281:40-46 (1979); EP 117,060; and EP 117,058.

15 4. Detecting Gene Amplification/Expression

Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to determine the transcription of mRNA (Thomas, Proc. Natl. Acad. Sci. USA 77:5201-5205 (1980)), dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled
20 probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the
25 duplex can be detected.

Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either
30 monoclonal or polyclonal and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence TRAG polypeptide or against a synthetic peptide based on the DNA sequences provided herein or against exogenous sequence fused to TRAG DNA and encoding a specific antibody epitope.

5. Purification of Polypeptide

Forms of TRAG may be recovered from culture medium or from host cell lysates.

Cells employed in expression of TRAG can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell lysing agents.

It may be desired to purify TRAG from recombinant cell proteins or polypeptides.

The following procedures are exemplary of suitable purification procedures: by

fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE;

chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; protein A Sepharose columns to remove contaminants such as IgG; and metal chelating columns to bind epitope-tagged forms of the TRAG. Various methods of protein purification may be employed and such methods are known in the art and described for example in Deutscher, Methods in Enzymology, 182 (1990); Scopes, Protein Purification: Principles and Practice, Springer-Verlag, New York (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular TRAG produced.

D. Uses for TRAG

Nucleotide sequences (or their complement) encoding TRAG have various applications in the art of molecular biology, including uses as hybridization probes, in chromosome and gene mapping, and in the generation of antisense RNA and DNA. TRAG nucleic acid will also be useful for the preparation of TRAG polypeptides by the recombinant techniques described herein. TRAG polypeptides have various applications in the art, including uses for evaluating factors that interact with and/or control TGF- β signaling as means for understanding both cell proliferation control and oncogenesis. Moreover, TRAG genes may be introduced into cells to effect mechanisms mediated by TGF- β as well as processes involved in oncogenesis.

30 1. Screening Methods Utilizing TRAG Nucleic Acids.

The full-length native sequence TRAG (Tables 1, 2, and 3) gene, or portions thereof, may be used as hybridization probes for a cDNA library to isolate, for instance, still other genes (like those encoding naturally-occurring variants of TRAG or TRAG

from other species) that have a desired sequence identity to the TRAG sequences disclosed in Tables 1, 2, or 3. Optionally, the length of the probes will be about 20 to about 500 bases. The hybridization probes may be derived from the nucleotide sequence or from genomic sequences including promoters, enhancer elements, and introns of native sequence TRAG. By way of example, a screening method will include isolating the coding region of the TRAG gene using the known DNA sequence to synthesize a selected probe of about 40 bases. Hybridization probes may be labeled by a variety of labels, including radionucleotides such as ^{32}P or ^{35}S , or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems. Labeled probes having a sequence complementary to that of the TRAG gene of the present invention can be used to screen libraries of human cDNA, genomic DNA, or mRNA to determine to which members of such libraries the probe hybridizes. Hybridization techniques are described in further detail in the Examples below.

Nucleotide sequences encoding a TRAG can also be used to construct hybridization probes for mapping the gene that encodes that TRAG and for the genetic analysis of individuals with genetic disorders. The nucleotide sequences provided herein may be mapped to a chromosome and specific regions of a chromosome using known techniques, such as *in situ* hybridization, linkage analysis against known chromosomal markers, and hybridization screening with libraries.

Screening assays can be designed to find lead compounds that mimic the biological activity of a native TRAG or a ligand or receptor for TRAG. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Small molecules contemplated include synthetic organic or inorganic compounds. The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays, and cell-based assays, which are well characterized in the art.

2. Modulation of TRAG protein Expression via TRAG Antisense Oligonucleotides.

Antisense technology entails the administration of exogenous oligonucleotides that bind to a target polynucleotide located within the cells. The term "antisense" refers to the fact that such oligonucleotides are complementary to their intracellular targets, e.g., TRAG. (See for example, Jack Cohen, OLIGODEOXYNUCLEOTIDES, Antisense

Inhibitors of Gene Expression, CRC Press, 1989; and Synthesis 1:1-5 (1988)). The TRAG antisense oligonucleotides of the present invention include derivatives such as S-oligonucleotides (phosphorothioate derivatives or S-oligos, see, Jack Cohen, supra), which exhibit enhanced cancer cell growth inhibitory action.

- 5 S-oligos (nucleoside phosphorothioates) are isoelectronic analogs of an oligonucleotide (O-oligo) in which a nonbridging oxygen atom of the phosphate group is replaced by a sulfur atom. The S-oligos of the present invention may be prepared by treatment of the corresponding O-oligos with 3H-1,2-benzodithiol-3-one-1,1-dioxide, which is a sulfur transfer reagent. See Iyer, R. P. et al, J. Org. Chem. 55:4693-4698
10 (1990); and Iyer, R. P. et al., J. Am. Chem. Soc., 112:1253-1254 (1990), the disclosures of which are fully incorporated by reference herein.

The TRAG antisense oligonucleotides of the present invention may be RNA or DNA which is complementary to and stably hybridizes with the first 100 N-terminal codons or last 100 C-terminal codons of the TRAG genome or the corresponding mRNA.

- 15 While absolute complementarity is not required, high degrees of complementarity are preferred. Use of an oligonucleotide complementary to this region allows for the selective hybridization to TRAG mRNA and not to mRNA specifying other regulatory subunits of protein kinase. Preferably, the TRAG antisense oligonucleotides of the present invention are a 15 to 30-mer fragment of the antisense DNA molecule having a
20 sequence that hybridizes to TRAG mRNA. Optionally, TRAG antisense oligonucleotide is a 30-mer oligonucleotide that is complementary to a region in the first 10 N-terminal codons and last 10 C-terminal codons of TRAG. Alternatively, the antisense molecules are modified to employ ribozymes in the inhibition of TRAG expression. (L.A. Couture & D. T. Stinchcomb, Trends Genet., 12: 510-515 (1996)).

- 25 In one embodiment, the TRAG antisense oligonucleotide is coadministered with an agent that enhances the uptake of the antisense molecule by the cells. For example, the TRAG antisense oligonucleotide may be combined with a lipophilic cationic compound that may be in the form of liposomes. The use of liposomes to introduce nucleotides into cells is taught, for example, in U.S. Pat. Nos. 4,897,355 and 4,394,448, the disclosures of
30 which are incorporated by reference in their entirety. See also U.S. Pat. Nos. 4,235,871, 4,231,877, 4,224,179, 4,753,788, 4,673,567, 4,247,411, and 4,814,270 for general

methods of preparing liposomes comprising biological materials. Alternatively, the TRAG antisense oligonucleotide may be combined with a lipophilic carrier such as any one of a number of sterols including cholesterol, cholate, and deoxycholic acid.

In another embodiment, the TRAG antisense oligonucleotide may be
5 coadministered with a second agent that is affected by TRAG expression. In one embodiment, this second agent is one or more isoforms of TGF- β . In a preferred embodiment, a combination of TRAG antisense oligonucleotides and TGF- β 1 are administered to cells that have reduced sensitivity to TGF- β due to TRAG overexpression. In this embodiment, a combination of these two molecules may be used
10 to synergistically induce TGF- β 1 mediated apoptosis. Methods pertaining to these embodiments are well known in the art. (Zwicker et al., Science, 271:1595-1597 (1996); Field et al., Cell, 85: 549-561 (1996); Slack et al., J. Cell Bio., 129: 779-788 (1995); Hiebert et al., Mol Cell Biol., 15: 6864-6874 (1995); White, E., Genes Dev., 10: 1-15 (1996); Martin et al., Cell, 82:349-352 (1995)).

15 The antisense oligonucleotides of the present invention may be prepared according to any of the methods that are well known to those of ordinary skill in the art. Preferably, the antisense oligonucleotides are prepared by solid phase synthesis. (See Goodchild, J., Bioconjugate Chemistry, 1:165-167 (1990)), for a review of the chemical synthesis of oligonucleotides. Alternatively, the antisense oligonucleotides can be
20 obtained from a number of companies that specialize in the custom synthesis of oligonucleotides.

3. Use of TRAG Nucleic Acids in the Generation of Transgenic Animals.

Nucleic acids that encode TRAG or its modified forms can also be used to
25 generate either transgenic animals or "knockout" animals which, in turn, are useful in the development and screening of therapeutically useful reagents. A transgenic animal (e.g., a mouse or rat) is an animal having cells that contain a transgene, which transgene was introduced into the animal or an ancestor of the animal at a prenatal stage, e.g., an embryonic stage. A transgene is a DNA that is integrated into the genome of a cell from
30 which a transgenic animal develops. In one embodiment, cDNA encoding TRAG can be used to clone genomic DNA encoding TRAG in accordance with established techniques and the genomic sequences used to generate transgenic animals that contain cells that

express DNA encoding TRAG. Methods for generating transgenic animals, particularly animals such as mice or rats, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009. Typically, particular cells would be targeted for TRAG transgene incorporation with tissue-specific enhancers.

- 5 Transgenic animals that include a copy of a transgene encoding TRAG introduced into the germ line of the animal at an embryonic stage can be used to examine the effect of increased expression of DNA encoding TRAG. Such animals can be used as tester animals for reagents thought to confer protection from, for example, pathological conditions associated with its overexpression. In accordance with this facet of the
- 10 invention, if an animal is treated with the reagent and a reduced incidence of the pathological condition is observed as compared to untreated animals bearing the transgene, this would indicate a potential therapeutic intervention for the pathological condition.

- Alternatively, nonhuman homologues of TRAG can be used to construct a TRAG
- 15 knockout animal that has a defective or altered gene encoding TRAG as a result of homologous recombination between the endogenous gene encoding TRAG and altered genomic DNA encoding TRAG introduced into an embryonic cell of the animal. For example, cDNA encoding TRAG can be used to clone genomic DNA encoding TRAG in accordance with established techniques. A portion of the genomic DNA encoding
- 20 TRAG can be deleted or replaced with another gene, such as a gene encoding a selectable marker that can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector (see e.g., Thomas and Capecchi, Cell, 51:503 (1987) for a description of homologous recombination vectors). The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and
- 25 cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected (see e.g., Li et al., Cell, 69:915 (1992)). The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras (see e.g., Bradley, in Teratocarcinomas and Embryonic Stem Cells: A Practical Approach, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152). A chimeric embryo
- 30 can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a knockout animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knockout animals can be characterized for instance,

for their ability to defend against certain pathological conditions and for their development of pathological conditions due to absence of the TRAG polypeptide.

4. Use of TRAG Upstream Control Sequences For Evaluating Neoplastic Processes

5 The genomic TRAG control sequences of the present invention, whether positive, negative, or both, may be employed in numerous various combinations and organizations to assess the regulation of TRAG. Moreover, in the context of multiple unit embodiments and/or in embodiments that incorporate both positive and negative control units, there is no requirement that such units be arranged in an adjacent head-to-head or head-to-tail
10 construction in that the improved regulation capability of such multiple units is conferred virtually independent of the location of such multiple sequences with respect to each other. Moreover, there is no requirement that each unit to comprise the same positive or negative element. All that is required is that such sequences be located upstream of and sufficiently proximal to a transcription initiation site.

15 To evaluate TRAG regulatory elements in the context of heterologous genes, one simply obtains the structural gene and locates one or more of such control sequences upstream of a transcription initiation site. Additionally, as is known in the art, it is generally desirable to include TATA-box sequences upstream of and proximal to a transcription initiation site of the heterologous structural gene. Such sequences may be
20 synthesized and inserted in the same manner as the novel control sequences. Alternatively, one may desire to simply employ the TATA sequences normally associated with the heterologous gene. In any event, TATA sequences are most desirably located between about 20 and 30 nucleotides upstream of transcription initiation.

 Preferably the heterologous gene is a reporter gene that encodes an enzyme that
25 produces colorimetric or fluorometric change in the host cell, which is detectable by in situ analysis and which is a quantitative or semiquantitative function of transcriptional activation. Exemplary enzymes include esterases, phosphatases, proteases (tissue plasminogen activator or urokinase), and other enzymes capable of being detected by activity that generates a chromophore or fluorophore as will be known to those skilled in
30 the art. A preferred example is *E. coli* beta-galactosidase. This enzyme produces a color change upon cleavage of the indigogenic substrate indolyl-B-D-galactoside by cells

bearing beta-galactosidase (*see, e.g.,* Goring et al., Science, 235:456-458 (1987) and Price et al., Proc. Natl. Acad. Sci. U.S.A., 84:156-160 (1987)). Thus, this enzyme facilitates automatic plate reader analysis of TRAG control sequence mediated expression directly in microtiter wells containing transformants treated with candidate
5 activators. Also, because the endogenous beta-galactosidase activity in mammalian cells ordinarily is quite low, the analytic screening system using β -galactosidase is not hampered by host-cell background.

Another class of reporter genes that confer detectable characteristics on a host cell are those that encode polypeptides, generally enzymes, which render their transformants
10 resistant against toxins, e.g., the neo gene, which protects host cells against toxic levels of the antibiotic G418; a gene encoding dihydrofolate reductase, which confers resistance to methotrexate; or the chloramphenicol acetyltransferase (CAT) gene (Osborne et al., Cell, 42:203-212 (1985)). Genes of this class are not preferred since the phenotype (resistance) does not provide a convenient or rapid quantitative output. Resistance to
15 antibiotic or toxin requires days of culture to confirm or complex assay procedures if other than a biological determination is to be made.

5. Use of TRAG Polypeptides in Protein-Protein Interaction Studies.

Co-immunoprecipitation and Gal4 protein-protein interaction assays may be
20 useful in screening for compounds modulating TRAG activity or in screening for compounds altering TRAG activity in a cell. For example, TRAG may participate with other WD repeat element-containing proteins in modulating TGF- β signaling. Those skilled in the art will understand that binding of a ligand at a molecular binding site can be modulated in a direct manner (e.g., by blocking the site), as well as altered in an
25 indirect manner (e.g., by conformational changes induced following binding of a second (different) ligand at a distant site). In this regard, it is likely that the binding site specificity of TRAG for a particular WD repeat element-containing protein can be completely altered (i.e., to bind a different ligand) by agents that bind at distant sites in these proteins. A number of exemplary protocols that may be used in these studies are
30 known in the art, *see e.g.* U.S. Patent No. 5,625,031.

Those skilled in the art will recognize that the functional regions of WD repeat element-containing proteins are particularly attractive targets for three-dimensional molecular modeling and for the construction of mimetic compounds, e.g., organic chemicals constructed to mimic the three-dimensional interactions between TRAG and another WD repeat element-containing protein. (See e.g., J. Wang, Curr Opin Gen. Dev., 7:39 (1997); Y. Taya et al., Trend Biochem. Sci., 22:14 (1997)).

6. Use of TRAG Containing Expression Vectors for Modulating Cellular Phenotype.

As discussed above, TRAG genes can be incorporated into any standard cloning vector. The term "vector" is well understood in the art and is synonymous with the often-used phrase "cloning vehicle." A suitable vector is a nonchromosomal double-stranded DNA comprising an intact replicon such that the vector is replicated when placed within a unicellular organism. Viral vectors include retroviruses, adenoviruses, adeno-associated virus (AAV), herpes virus, papovirus, adeno-retrovirus, etc. Other suitable vectors include plasmids. Plasmids and retroviruses are generally preferred as vectors.

As discussed in Example 8, pcDNA3.1-TRAG (pcDNA3.1 purchased from Invitrogen) was constructed and contained the CMV promoter. This promoter is suitable for expression of the TRAG genes in a wide variety of cells. However, the CMV promoter is not specifically required for transcription and expression of the TRAG genes. The CMV promoter can be replaced with other known promoters to improve the efficiency of transcription and expression in particular cells.

The promoter DNA can be amplified using PCR technology while concurrently providing restriction sites at the 5' and 3' ends of the promoter DNA. The amplified promoter DNA can then be inserted into a cloning vehicle (for example pcDNA3.1) using conventional endonucleases and known recombinant DNA technology. Cloning vectors containing the desired promoter upstream of the 5' end of TRAG genes may be constructed in this manner.

Cellular phenotype can be influenced by using the TRAG gene. In this context, cloning vectors containing an appropriate promoter and the TRAG gene may be constructed using PCR technology in a manner analogous to the preparation of vectors

containing exogenous genes as is well known in the art. Cloning vectors containing TRAG genes are transfected into host cells using known transfection processes. Suitable transfection processes include lipofection, electroporation, and retrovirus infection. When transfecting cells with TRAG, the desired cells are isolated and cultured in suitable media.

Transfection of cells using lipofection may be conducted according to standard lipofection procedures. (See Felgner et al., Proc. Natl. Acad. Sci. (USA), 84:7413-7417 (1987)). In general, liposome-mediated DNA transfection is accomplished by exposing 1-20 micrograms of plasmid DNA and commercially available liposomes (Bethesda Research Laboratories) in culture medium. The transfected cells are then repeatedly passaged in culture medium and the desired clones are isolated.

Retrovirus infection may also be accomplished using previously described procedures. (See, for example, Miller et al., J. Virol., 62:4337-4345 and Halbert et al., J. Virol., 65:473-378 (1991)). In general, plasmid DNA is transfected into a desired packaging cell line such as Psi-2 or other cell lines, using standard calcium phosphate precipitation. Viruses produced from the Psi-2 cells or equivalent cells are then used to infect an amphotropic packaging cell line, for example PA317. Viruses produced by the amphotropic packaging cell line are used to infect the desired host parent cells of the present invention.

Selection of clones with a modulated phenotype may be undertaken by a variety of protocols that are well known in the art (see e.g. U.S. Patent No. 5,376,542). In such selections, the cells may be selected for their ability to respond to factors such as TGF- β . Alternatively, cells can be selected by their ability to form colonies and grow in soft agar. Moreover, the cells can be selected by their ability to form tumors in animal models such as in nude mice. Similarly, cancer cells or cells having aggressive metastasis can be selected.

After transfection, the desired clones are selected by culturing in optimal media and repeated passaging. Generally, 10-20 passages are required to eliminate spurious cells and obtain pure clonal cells. Optimal media are selected according to the type of parent cell that is utilized. For lymphocytes, RPMI media is preferred; for fibroblasts,

DMEM media is preferred; and for epithelial cells, a serum-free medium such as keratinocyte growth medium (KGM) or SFM (Gibco Company) is preferred.

Selected colonies are then tested to verify the presence of TRAG DNA and the expression of TRAG genes. Verification is confirmed by standard Southern hybridization techniques and immunoprecipitation to determine the presence or quantity of expressed TRAG proteins.

7. Chromosomal Localization.

In Example 2, chromosomal localization of the human and murine TRAG genes is described. Chromosomal localization was done by FISH analysis (Stokke, T. et al., Genomics, 26: 134-137 (1995)). Murine TRAG maps to chromosome 18, and human TRAG maps to chromosome 18.

In other embodiments the invention provides diagnostic assays for determining chromosomal rearrangement of TRAG genes in a cell. The chromosomal location of TRAG genes is conveniently determined in chromosomal smears by *in situ* hybridization with oligonucleotide probes or cDNA and the like. Translocation of a TRAG gene, i.e., from a chromosomal location found in a normal cell to a location found in a transformed cell, may contribute to a phenotype of uncontrolled cell growth by removing normal transcription regulatory control of expression of TRAG. In the case where the rearrangement induces overexpression, the cell may acquire a malignant (i.e., uncontrolled) growth phenotype, and in the case where the rearrangement induces underexpression, the cell may undergo premature senescence. Screening cellular samples from individuals for the potential of TRAG chromosomal rearrangement may indicate a relative risk factor for the possibility of developing cancer.

E. Anti-TRAG Antibodies

The present invention further provides anti-TRAG antibodies. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

1. Polyclonal Antibodies

The TRAG antibodies may comprise polyclonal antibodies. Methods of

preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the TRAG polypeptide or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants that may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). Further, polyclonal antibodies may be generated commercially, for example by Genemed Synthesis, Inc. using art-accepted methods.

2. Monoclonal Antibodies

The TRAG antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, *Nature*, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*.

The immunizing agent will typically include the TRAG polypeptide or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if nonhuman mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (Goding, *Monoclonal Antibodies: Principles and Practice*, Academic Press, (1986) pp. 59-103). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine, and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin,

and thymidine ("HAT medium"), which are substances that can prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies (Kozbor, J., Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63).

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against TRAG. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980).

After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods (Goding, *supra*). Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells may be grown *in vivo* as ascites in a mammal. The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography. The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into

host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also may be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences (U.S. Patent No. 4,816,567) or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a nonimmunoglobulin polypeptide. Such a nonimmunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

The antibodies may be monovalent antibodies. Methods for preparing monovalent antibodies are well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy chain crosslinking.

Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking. *In vitro* methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art.

3. Humanized Antibodies

The TRAG antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of nonhuman (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains, or fragments thereof (such as Fv, Fab, Fab', F(ab')₂, or other antigen-binding subsequences of antibodies) that contain minimal sequence derived from nonhuman immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary-determining region (CDR) of the recipient are replaced by residues from a CDR of a nonhuman species (donor antibody) such as mouse, rat, or rabbit having the desired specificity, affinity, and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding nonhuman residues. Humanized antibodies may also comprise residues that are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized

antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a nonhuman immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also
5 will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)).

Methods for humanizing nonhuman antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it
10 from a source that is nonhuman. These nonhuman amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and coworkers (Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)), by substituting
15 rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a nonhuman species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and
20 possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)). The techniques of Cole et al. and
25 Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, p. 77 (1985) and Boerner et al., J. Immunol., 147(1):86-95 (1991)).

Humanized antibodies can also be prepared according to the methods disclosed by, for example, U.S. Patent Nos. 5,175,384; 5,434,340; 5,545,806; 5,569,825;
30 5,591,669; 5,625,126; 5,633,425; 5,916,771; and 5,589,369.

4. Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one

of the binding specificities is for the TRAG, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit. Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuello, Nature, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., EMBO J., 10:3655-3659 (1991).

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors and are cotransfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

5. Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Patent No. 4,676,980) and for treatment of HIV infection (WO 91/00360; WO 92/200373; EP 03089). It is contemplated that the antibodies may be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

F. Uses for TRAG Antibodies

The TRAG antibodies of the invention have various utilities. For example, TRAG antibodies may be used in diagnostic assays for TRAG, *e.g.*, detecting its expression in specific cells, tissues, or serum. Various diagnostic assay techniques
5 known in the art may be used, such as competitive binding assays, direct or indirect sandwich assays, and immunoprecipitation assays conducted in either heterogeneous or homogeneous phases (Zola, Monoclonal Antibodies: A Manual of Techniques, CRC Press, Inc. (1987) pp. 147-158). The antibodies used in the diagnostic assays can be labeled with a detectable moiety. The detectable moiety should be capable of producing,
10 either directly or indirectly, a detectable signal. For example, the detectable moiety may be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the detectable moiety may be employed,
15 including those methods described by Hunter et al., Nature, 144:945 (1962); David et al., Biochemistry, 13:1014 (1974); Pain et al., J. Immunol. Meth., 40:219 (1981); and Nygren, J., Histochem. and Cytochem., 30:407 (1982). In addition, TRAG or antibodies that recognize TRAG may be used in drug screening assays to identify compounds that act to positively or negatively modulate the function of TRAG.

20 The antibodies can also be TRAG antagonists or agonists. Antibodies may also be useful therapeutically either alone, as agents that would act directly to interfere with the function of TRAG or indirectly as targeting agents capable of delivering a toxin, for example, pseudomonas exotoxin or radioisotopes, conjugated thereto to a desired site.

TRAG antibodies also are useful for the affinity purification of TRAG from
25 recombinant cell culture or natural sources. In this process, the antibodies against TRAG are immobilized on a suitable support, such a Sephadex resin or filter paper, using methods well known in the art. The immobilized antibody then is contacted with a sample containing the TRAG to be purified, and thereafter the support is washed with a suitable solvent that will remove substantially all the material in the sample except the
30 TRAG, which is bound to the immobilized antibody. Finally, the support is washed with another suitable solvent that will release the TRAG from the antibody.

The following examples are offered for illustrative purposes only and are not

intended to limit the scope of the present invention in any way. All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

EXAMPLES

Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, 10801 University Boulevard, Manassas, Virginia, USA.

EXAMPLE 1

Isolation of Rat TRAG cDNA and Determination of Tissue Expression

Loss of TGF- β 1 induced growth inhibition is an early event during spontaneous transformation of RLE cells. (A.C. Hugget et al., Cancer Res., 51:5929 (1991)). This resistance to the growth inhibitory effects of TGF- β 1 can be caused by multiple factors. (E.R. Barrack, Prostate, 31:61 (1997); R.W. Padgett et al., Cytokine Growth Factor Rev., 8:1 (1997); L. Attisano, et al., Cytokine Growth Factor Rev., 7:327 (1996)). However, we observed a number of the transformed cell lines displaying resistance to the growth inhibitory effects of TGF- β 1 that apparently had a "normal" number of TGF- β receptors. (A.C. Hugget et al., Cancer Res., 51:5929 (1991)). These observations suggested a post-receptor disruption of the growth inhibitory signal(s) of TGF- β 1. To search for endogenous genes that confer resistance to the growth inhibitory effects of TGF- β 1, and which in turn may lead to cellular transformation, subtractive hybridization (J.T. Woitach et al., Nat. Genet., 19:371 (1998)) was done on two rat liver epithelium (RLE)-derived cell lines that were sensitive (RLE phi 13) or insensitive (B5T) to TGF- β . (For a discussion about the production of RLE phi 13 and B5T cell lines, see A.C. Huggett et al., Cancer Research, 51:5929 (1991)). B5T designates a cell line derived from an RLE parent line by multiple passages (i.e. allowing cells to grow to fill a culture plate (confluency), and then diluting these cells into a fresh plate and allowing them to once again reach confluency). Unlike RLE phi 13 cells, B5T cells are insensitive to TGF- β and exhibit a transformed phenotype.

A novel transcript, TRAG (TGF- β Resistance Associated Gene), was identified and shown to be overexpressed in the B5T cells as well as one other transformed RLE line (C4T) derived in an identical way to B5T (A.C. Huggett et al., Cancer Research, 51:5929 (1991)), both of which are resistant to the effects of TGF- β 1 (Figure 1).

5

Isolation of Rat TRAG cDNA

To isolate rat TRAG cDNA, poly-A⁺ was first isolated from RLE phi 13 cells and B5T cells by using oligo (dt) cellulose, as previously described (Bradley JE, Bishop GA, St John T, Frelinger JA, Biotechniques, 6:114-116 (1988)). The cDNAs were
10 synthesized using SuperScript reverse transcriptase (BRL) as recommended by the vendor; added with BstXI adaptor (InVitrogen); and used to produce RLE phi 13 and B5T cDNA libraries in pcDNAneo.

For B5T cDNA enriched subtractive cDNA library construction, B5T and RLE phi 13 cDNAs were digested with HindIII+XbaI and BamHI+XhoI, respectively, and
15 subjected to agarose gel purification. Digested RLE phi 13 cDNA fragments (20 μ g) were digested further with AluI+RsaI and dephosphorylated, then hybridized with HindIII+XbaI digested B5T cDNA fragments (0.4 μ g). The hybridization mixture was used to construct the B5T cDNA enriched subtractive cDNA library in BluescriptM13 with HindIII+XbaI protruding termini. The enriched library was plated and single
20 colonies were isolated. The plasmid from each clone/colony was sequenced, and novel sequences were used to screen a panel of rat tumor samples and synchronized cells. A 0.8kb cDNA clone encoding part of the 3' untranslated region (3'UTR) of the TRAG gene was isolated. This clone was picked for its overexpression in B5T cells, relative to RLE cells, following screening by Northern hybridization techniques, and for its novel
25 sequence. The single similar (homologous) sequence that was found in the sequence databases represented an uncharacterized cDNA clone from human brain, identified by the name KIAA0541 (GenBank Accession Number AB011113). Using primers designed against this sequence, and making use of reverse transcriptase (RT)-PCR and sequencing, the remainder of the 3' untranslated region and part of the coding region were isolated
30 and characterized from rat (Table 1). RT-PCR describes a molecular biology technique by which isolated single-stranded complementary DNA (cDNA) is produced from total

mRNA or poly-A⁺ RNA using the Reverse Transcriptase enzyme (SuperScript II from Gibco, BRL Life Technologies). This cDNA can then be used as a template for amplification in a PCR reaction. The template for RT-PCR was total RNA isolated from B5T cells (derived from RLE parent cells) or fresh brain tissue from rat.

5 The remainder of the coding region of rat TRAG, in particular, ~2kb of the 5' upstream region (including the transcription and translation start sites) was obtained using the RACE (random amplification of cDNA ends) technique, as described in the manufacturer's instructions accompanying the SMART[®] RACE kit (Clontech, Palo Alto, CA). The human TRAG sequence homologous to this region was *not* present in the
10 KIAA0541 clone.

Sequence specific to rat brain TRAG cDNA was isolated as described above from cDNA obtained by RT (reverse transcriptase) experiments using total RNA extracted from Fisher F344 rat brain tissue (Table 1, bases 2876-2968).

15 The final size of the coding region for rat TRAG cDNA was 4,464 base pairs, encoding a protein of 1,488 amino acids.

Plasmids and PCR products were sequenced using the BigDye Terminator Ready Reaction Kit (cat# 4303149, Perkin-Elmer Applied Biosystems). The reactions were purified using Centrifac Gel Filtration Columns (cat# 42453, Edge Biosystems, Inc.). The samples were analyzed on a 377 ABI Prism DNA sequencer (Perkin-Elmer Applied
20 Biosystems) to determine the primary nucleotide sequence. The predicted amino acid sequence having 1,488 amino acids (with a predicted Mr ~ 165,000 Daltons) was then derived using PCGENE. The derived amino acid sequence is indicated by the 3-letter code below the corresponding bases in Table 1.

25 Isolation of Mouse TRAG cDNA

The mouse TRAG gene was isolated by RT-PCR and RACE-PCR as described above for the rat TRAG gene, except that the primers used were designed against the rat TRAG sequence (which is closer to mouse TRAG than human is). Brain-specific
sequence (Table 3, bases 2876-2971) was obtained as outlined above, using brain tissue
30 from the SvJ129 mouse strain. Mouse genomic clones were isolated by screening a mouse BAC genomic libraries from the SvJ strain of mouse (performed by Genome

Systems, Inc.). The template for RT-PCR was total RNA isolated from fresh liver or brain for mouse. The template derived from mouse brain was used to sequence cDNA specific to brain tissue, which contained an additional coding region not found in the liver. The template derived from mouse liver was used to sequence cDNA specific to
5 liver, which was shown to lack that coding region present in brain tissue.

The mouse cDNA sequence was determined as described above for rat cDNA. A cDNA clone having 4,467 base pairs was generated from mouse by RT-PCR and RACE-PCR (Table 3).

The predicted amino acid sequence having 1,489 amino acids (with a predicted
10 Mr ~ 165,000 Daltons) was then derived using PCGENE. The derived amino acid sequence is indicated by the 3-letter code below the corresponding bases in Table 3.

Isolation of Human TRAG cDNA

The human TRAG gene was isolated from human poly-A⁺ RNA obtained
15 commercially from Clontech (cat# 6510-1, Palo Alto, CA) by RT-PCR, as described above, but using human-specific oligonucleotide primers which were obtained from sequence data deposited in GenBank for KIAA0541 (Accession Number AB011113). These primers were chosen because this GenBank sequence showed homology to the 3'UTR of the cDNA clone derived from the B5T cell described above for the isolation of
20 the rat TRAG sequence. However, this human sequence (KIAA0541) was incomplete, lacking the 5' ~1.5 to ~2kb of the TRAG gene, including the transcription and translation start sites. The sequence of this missing region was determined by searching GenBank with the relevant mouse sequence (i.e. the first ~2kb of the mouse TRAG gene). This search yielded an uncharacterized genomic clone from chromosome 18 (containing both
25 intronic and exonic sequence from the 5'-most region of the TRAG gene). By comparing mouse TRAG cDNA to this human genomic sequence, it was possible to detect the human exonic sequences and assemble them into a recognizable cDNA sequence. The entire human TRAG sequence was confirmed using RT-PCR of human poly-A⁺ RNA (see above) and sequencing. The exon specific to brain, which was present in the
30 KIAA0541 sequence, can be found in Table 2, bases 2924-3022.

A cDNA clone having 4,470 base pairs was generated from human by RT-PCR (Table 2). The predicted amino acid sequence having 1,490 amino acids (with a predicted Mr ~ 165,000 Daltons) was then derived using PCGENE. The derived amino acid sequence is indicated by the 3-letter code below the corresponding bases in Table 2.

- 5 The comparison of the cDNA sequence of TRAG from human, mouse, and rat indicates that TRAG is a highly conserved gene in all of these species, as is the amino acid sequence (Table 4).

Characterization of TRAG cDNA and Protein

- 10 DNA homology searches of GenBank revealed TRAG to be a unique transcript. Yet some homologous sequences were identified. A cDNA clone from human brain (KIAA0541, GenBank Accession No. AB011113) having approximately 87% nucleotide homology with the mouse TRAG gene was identified. A putative Drosophila G-protein subunit (GenBank Accession No. AL021086) having approximately 52% homology with
15 the mouse TRAG protein was also identified using the BLAST search program. This homology is shown in Table 5. We compared the deduced amino acid sequence of TRAG with known proteins in the Swissprot database. TRAG contains no domains similar to other proteins. However, the deduced protein sequence does contain 4 WD repeat motifs (Tables 1, 2 and 3, underlined).

- 20 Based on the identification of the WD repeat motifs, TRAG may interact with the TGF- β pathway through these WD repeat motifs in a way similar to TRIP-1 and STRAP. Considering the means by which TRAG was isolated (i.e. by virtue of its overexpression in TGF- β resistant cells), it could play an important role in the TGF- β pathway and upregulation may interfere with normal TGF- β signaling. TRAG may
25 interact directly with one of the TGF- β receptors and/or with another WD repeat-containing protein in the pathway, for example TRIP-1 and/or STRAP. We have already demonstrated an association of TRAG overexpression with a loss of TGF- β sensitivity and with an aggressive and malignant phenotype (see Examples below).

TRAG Expression

The expression of TRAG in three types of rat cells (B5T, RLE phi 13, and C4T) was analyzed by Northern blot (Figure 1A) to determine whether any difference in expression existed in the transformed (TGF- β resistant) cell lines relative to the nontransformed (TGF- β sensitive) RLE phi 13 cell line.

To determine TRAG expression levels in certain rat cells, RNA was first isolated from 3 rat cell lines (transformed B5T, transformed C4T, and untransformed RLE cells) (A.C. Huggett, et al., Cancer Res., 51:5929 (1991)), poly-A⁺ mRNA selected using oligo (dt) cellulose (Bradley JE, Bishop GA, St John T, Frelinger JA (1988), Biotechniques, 6:114-116), and 5 μ g (10 μ g of total RNA) was then fractionated under denaturing conditions by electrophoresis on a 1% agarose gel, containing formaldehyde (0.22 M) and 1x MOPS (50 mM 3-[N-morpholino] propanesulfonic acid and 1mM EDTA). Samples were electrophoresed for about 3 hours at 80V, blotted overnight onto nitrocellulose membranes, and cross-linked under ultraviolet light. Membranes were prehybridized in QuikHyb (Stratagene, La Jolla, CA) for 15 minutes at 68°C, labeled probe (0.8kb dsDNA against part of the 3'UTR; about 1x10⁶ cpm/ml) was added, and the membrane and probe were incubated for about 60 minutes at 68°C. The membrane was washed and then exposed to phosphorimager plates for 48 hours. The results are shown in Figure 1A.

The expressed TRAG levels were then quantified (Figure 1B). The results indicate that TGF- β resistant B5T cells express higher levels (up to 7 fold) of TRAG than do RLE phi 13 cells.

EXAMPLE 2

Chromosomal Localization of TRAG in Mouse and Human

Chromosomal localization of TRAG in mouse and human was done by FISH analysis (Stokke, T., Collins, C., Kuo, W., Kowbel, D., Shadravan, F., Tanner, M., Kallionienmi, A., Kallioniemi, O., Pinkel, D., Deaven, L., and Gray, J ; A physical map of chromosome 20 established using fluorescent in situ hybridization (FISH) and digital image analysis, Genomics, 26: 134-137 (1995)). A FISH analysis generally involves probing chromosomes with a labeled DNA. The probes used to localize TRAG on

mouse and human chromosomes were prepared by labeling purified mouse and human DNA, respectively, with biotin (Random-Prime labeling kit: Boehringer-Mannheim Corp., Indianapolis, IN).

To localize TRAG on the mouse chromosome, a unique BAC clone (BAC21521) isolated from a 129SvJ mouse kidney library was used as a probe. This BAC clone was isolated by using a probe to the 3' untranslated region (UTR) of the rat TRAG gene (screening performed commercially by Genome Systems, Inc., St. Louis, MO).

To localize TRAG on the human chromosome, a ~5kb DNA probe complementary to the central portion of the human TRAG gene (exons 12-14, including intervening introns), obtained by PCR amplification of human genomic DNA, was used.

The biotin-labeled DNA probe was hybridized *in situ* to chromosomes derived from normal methotrexate-synthesized peripheral leukocyte cultures for human and to chromosomes derived from normal spleen cells in the case of mouse. Overall, forty-eight cells were studied.

The conditions used for hybridization, processing, analysis, direct fluorescent signal localization, and banded chromosomes have been described previously in detail (Zimonjic et al., Cytogenet. Cell Genet., 65:184 (1994)).

The TRAG gene was localized to chromosome 18D.1-E.3 in the mouse (see Figure 2A) and to chromosome 18q21.1-22 in the human (see Figure 2B).

The long arm of human chromosome 18, designated 18q, and particularly the distal end of that region, has been found to be involved in a number of cancers and developmental disorders. The 18q region contains a number of genes which have been shown to play an integral role in various tumorigenic pathways by deletion studies. These genes include DCC (deleted in colorectal cancer) (L. Hendrick, et al., Genes Dev., 8:1174 (1994)), BCL-2 (Y Tsujimoto et al., Science, 228:1440 (1985)), and DPC4 (deleted in pancreatic cancer) (SA Hahn et al., Science, 271:350 (1996)). TRAG sits between DCC and BCL-2 on chromosome 18q, a region that has also been shown to potentially be involved in a chromosomal rearrangement-associated mucosa-associated lymphoid tissue (MALT) lymphomas. (A Stoffel et al., Genes Chromosomes Cancer, 24:156 (1999)).

Inherited monosomy of 18q (i.e. loss of only one allele, so-called "18q- syndrome") has been associated with a variety of developmental and physiological defects, particularly those of the brain. (AD Kline et al., Am. J. Hum. Genet., 52:895

(1993)). Associated with 18q⁻ syndrome are various dysmorphic features as well as a string of neurological and other brain abnormalities, including microcephaly and abnormal MRI. (AD Kline et al., Am. J. Hum. Genet., 52:895 (1993)). The severity of defects appears to be correlated with the extent of the 18q deletion involved. For example, patients studied with deletions in the region of the TRAG gene showed more severe defects, particularly of brain development, than those carrying deletions that did not incorporate this area of the chromosome. (AD Kline et al., Am. J. Hum. Genet., 52:895 (1993)). This circumstantial evidence, coupled with the data showing the highest levels of TRAG expression in the brain (see Example 3), leads us to conclude that beyond a role in carcinogenesis, the TRAG gene may play a vital role in brain and mental development.

EXAMPLE 3

Determination of Expression of TRAG

To determine the normal expression of TRAG, a commercial multiple tissue RNA blot from rat (Clontech, Palo Alto, CA) was probed, utilizing Northern blotting techniques, with a radioactively labeled TRAG probe as described in Example 1.

The results are shown in Figure 3A. Figure 3A shows TRAG mRNA having a transcript size of 7.2 kb in spleen, lung, liver, muscle, and kidney, and TRAG mRNA having a transcript size of 3.5 kb in the testis. TRAG mRNA having a variety of transcript sizes (arrow heads in Figure 3A) was identified in brain suggesting alternative splicing.

Other TRAG expression tests were conducted using mouse and human dot blot membranes (Clontech, Palo Alto, CA), utilizing the identical Northern blot analysis protocol as detailed in Example 1, except that different probes were used. For human tissues, a probe of approximately 1.5 kb of human TRAG from the 5' end of the gene was used, and for mouse tissues, a probe of approximately 2.5 kb of mouse TRAG from the center of the gene was used.

Figure 3B shows the results for expression in human and Figure 3C shows the results for expression in mouse. Although the commercial multiple tissue RNA blot from rat did not show TRAG mRNA in heart (Figure 3A), the dot blot corresponding to expression in human did show mRNA for TRAG in heart (Figure 3B). The dot blot
5 showed the most abundant TRAG mRNA expression in brain (Figures 3B and 3C). The dot blot also showed TRAG mRNA in all fetal tissues as well as all tissues during embryonal development (Figures 3B and 3C).

EXAMPLE 4

10 Analysis of TRAG Protein

To evaluate the expression of TRAG protein, protein extracts from three rat cell lines were studied (RLE phi 13, B5T, and C4T) by Western blot. Protein (40 µg) from each of the cell lines was collected by lysis of cells in RIPA lysis buffer (1% Tergitol NP-40, 0.5% sodium deoxycholate, 0.1% SDS, in 1X PBS). Inhibitors were added just
15 before use (Complete, Mini; Boehringer-Mannheim, Burlingame, CA) according to manufacturer's instructions. Lysis buffer was added to plates after a brief wash with 1X PBS (containing inhibitors), cells were scraped from the plate and placed on ice for 5 minutes. After passing lysate through a 22 gauge syringe needle, samples were centrifuged at 4°C and 14,000g for 30 minutes. The supernatant was collected as crude
20 extract and the protein concentration determined using the Bio-Rad Protein Assay (Bio-Rad, Hercules, CA). This protein (30µg to 40µg) was electrophoresed for 2.5h, 80V at room temperature on a polyacrylamide gel using a Novex XCell II Mini-cell System (Novex, San Diego, CA), according to manufacturers instructions, and then blotted onto nitrocellulose (25V, 2 hours). The nitrocellulose was incubated in a solution of 5% non-fat milk powder (NFMP), 3% BSA (bovine serum albumin), and 0.5% Tween-20 in
25 Tris-buffered saline (TBS) for 1 hour at room temperature, washed 3 times in TBS + 0.05% Tween-20 (TBS-T), and placed in a solution of 5% NFMP, 3% BSA, and TBS-T (1°/2° Antibody Solution). To this was added the primary rabbit anti-TRAG antibody (1:1000 dilution; production of antibody described in Example 7) and the membrane
30 incubated overnight at 4°C. After 3 TBS-T washes, secondary antibody (anti-rabbit horse radish peroxidase (HRP)-conjugated IgG; Santa Cruz Biotechnology, Santa Cruz, CA) was applied to the membrane in the same 1°/2° Antibody Solution used for the

primary antibody. Incubation was one hour at room temperature. After 3 TBS-T washes, the membrane was placed in ECL solution (Amersham, Arlington Heights, IL) for 1 minute, according to the supplied protocol, followed by exposure to Kodak X-Omat AR film for between 30 seconds and 2 minutes. The primary polyclonal anti-TRAG antibody that was used was raised in a rabbit against a peptide from the TRAG protein. This was done commercially by Genemed Biotechnologies Inc., San Francisco, CA, as described in Example 7.

The results are shown in Figure 4. Figure 4 shows TRAG protein expressed in all three cell lines. Yet B5T and C4T show greater amounts of protein than RLE phi 13. The TRAG protein appears to be about 100 kDa to about 105 kDa. Although this molecular weight is not immediately compatible with a coding sequence of approximately 4.4 kb (see Table 1), it is believed that alternative splicing produces a transcript of between about 3.3 kb and about 3.5 kb.

EXAMPLE 5

Determination of the Status of TRAG in Tumor Cell Lines

To determine the status of TRAG in tumor cell lines, protein extract and mRNA extract from a variety of tumor cell lines were studied by Western blot and Northern blot, respectively. In one study, protein extract and mRNA extract from cells that were chemically transformed using aflatoxin or virally transformed were examined. The chemically transformed cells were AFL-B8 and AFL-D8, and the virally transformed cells were 3611T2, 3611T5, and J2-14. These cells were produced in our laboratory according to JB McMahon et al., Cancer Res., 46:4665 (1986) and AC Huggett et al., Cancer Res., 51:5929 (1991). The levels of TRAG protein and mRNA in these cells were compared to levels of TRAG mRNA and protein in RLE phi 13 and B5T cells.

To determine TRAG protein level in these cells, a Western blot was conducted. Protein (40 µg) was isolated from each of the cell lines as described above in Example 4. The isolated protein was electrophoresed on a polyacrylamide gel and blotted onto nitrocellulose according to the methods described in Example 4. The nitrocellulose was then probed with the polyclonal antibody (1: 1,000 dilution) according to Example 4. The results are shown in Figure 5A. The level of TRAG protein correlated with the aggressiveness and metastatic ability of the particular cell lines. For example, J2-14, which is a highly aggressive metastatic tumor cell line transformed with *c-raf* and *v-myc*, shows the highest level of TRAG protein, while 3611T2, which is metastatic, shows

a level of TRAG protein that is greater than 3611T5, which is nonmetastatic. Aggressiveness and metastatic ability were determined by observation of tumors following injection into nude mice (PJ Worland, et al., Mol. Carcinog., 3:20-29 (1990)).

To determine TRAG mRNA level in these cells, a Northern blot was conducted,
5 as described above in Example 1. The results are shown in Figure 5A.

In another study, protein extract and mRNA extract from tumor cell lines derived from double transgenic *c-myc/TGF- α* mice (i.e., 221T1, 223B.3, 241T1, 241T3, and 263B.1) were evaluated. To determine TRAG protein level in these cells, a Western blot was conducted as described above. In this blot, the cancer cell lines were compared to
10 B5T cells and to RLE phi 13 cells. The results are shown in Figure 5B. As for the transformed rat cell line, TRAG protein levels can be seen to be greatly elevated in these cells relative to RLE, and at comparable levels to B5T. This data strengthens the association between high TRAG levels and a transformed phenotype.

To determine TRAG mRNA level in these cells, a Northern blot was conducted
15 as described above. The results are shown in Figure 5B.

In another study, protein extract and mRNA extract from the following human tumor cell lines were evaluated: Alex, Chang, FOCUS, HepG2, Huh-7, Sk-Hep-1, WRL-68, and HeLa. To determine the level of TRAG protein, a Western blot as described above was conducted. The results are shown in Figure 5C. Figure 5C shows a
20 significant increase in TRAG protein in HepG2, which is an aggressive, transformed cell line.

To determine TRAG mRNA level in these cells, a Northern blot was conducted as described above. The results are shown in Figure 5C.

In yet another study, protein extract and mRNA extract from fresh, primary
25 tumors taken from live double transgenic *TGF- α /c-myc* mice were evaluated and compared to the corresponding levels in RLE phi 13 and B5T cells. Figure 5D shows that liver tumors from double transgenic *TGF- α /c-myc* mice have elevated levels of TRAG protein relative to RLE phi 13. Approximately 75% of the primary liver tumors (T) isolated from *TGF- α /c-myc* mice showed higher levels of TRAG protein than did
30 normal tissue (N) (Figure 5D).

EXAMPLE 6

The Determination of Cellular Localization of the TRAG Protein

The cellular localization of the TRAG protein was determined by confocal

microscopy. To make this determination, RLE phi 13 and B5T cells were transfected with empty (i.e. no TRAG insert) green fluorescent protein (GFP) vector (Clontech, Palo Alto, CA). These cells acted as the control. Other RLE phi 13 and B5T cells were transfected with the N-terminal GFP protein vector also containing the TRAG gene. This
5 N-terminal fusion protein vector was constructed by inserting an EcoRI/SalI fragment encoding full-length TRAG into the pEGFP-N2 vector (Clontech, Palo Alto, CA) containing the green fluorescent protein (GFP). Transfection was carried out using LipofectAMINE PLUS reagent (Gibco, BRL Life Technologies, Rockville, MD), according to manufacturer's instructions. Microscopy conditions were: 20X zoom and
10 3% laser power (for B5T) or 10% laser power for RLE phi 13. The results are shown in Figures 6A and 6B.

Cells transfected with empty (pEGFP-N2) vector displayed GFP signal over the entire cell (Figures 6A, panels under "GFP-only"). But cells having the TRAG-GFP fusion protein vector showed only cytoplasmic fluorescence (Figure 6A, panels under
15 "TRAG-GFP").

The cellular localization of the TRAG protein was confirmed by immunohistochemistry. Immunohistochemistry was conducted according to the standard procedures described in E. Harlow and D. Lane, "Using Antibodies: A Laboratory Manual," Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY (1999). In
20 particular, the TRAG protein in paraformaldehyde-fixed RLE phi 13 and B5T cells was probed using anti-TRAG polyclonal antibody (1:1,000 dilution). The polyclonal antibody was prepared according to Example 4. The results are shown in Figure 6B. Figure 6B shows that the TRAG protein localizes to the cytoplasm, but not to the nucleus. In fact, strongest staining is seen *around* the nucleus, within the cytoplasm (i.e.
25 perinuclear).

These results were compared to staining for pre-immune (PI) serum as a negative control. PI serum describes the serum removed from the rabbit *before* it is immunized. That is, before the rabbit was challenged with the TRAG polypeptide and induced to make the anti-TRAG antibody. Figure 6B shows significantly lighter staining for pre-
30 immune serum than for RLE phi 13 and B5T cells.

EXAMPLE 7

Preparation of Antibodies that Bind TRAG

Polyclonal antibodies to TRAG were generated commercially by Genemed Synthesis, Inc. using art-accepted methods. Initially, the rabbits were immunized with a polypeptide corresponding to amino acids 760-781 of the rat TRAG sequence (Table 1). Subsequent Western Blot experiments (Example 4) showed that the anti-TRAG antibody cross-reacted well with both mouse and human TRAG.

The following example illustrates preparation of monoclonal antibodies that can specifically bind TRAG.

Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, *supra*. Immunogens that may be employed include purified TRAG, fusion proteins containing TRAG, and cells expressing recombinant TRAG on the cell surface. Selection of the immunogen can be made by the skilled artisan without undue experimentation.

Mice, such as Balb/c, are immunized with the TRAG immunogen emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, MT) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect TRAG antibodies.

After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of TRAG. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

The hybridoma cells will be screened in an ELISA for reactivity against TRAG. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against TRAG is within the skill in the art.

The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-TRAG monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished
5 using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

EXAMPLE 8

10 Cloning of mouse TRAG gene in pcDNA3.1⁺

The full length mouse TRAG gene was cloned into pcDNA3.1⁺ vector in three parts: a 5' EcoRI/Cla I fragment, a central ClaI/XhoI, and a 3' XhoI/XbaI fragment. In all cases, PCR-amplified fragments were cloned into pGEM[®]-T Easy vectors (Promega, Madison, WI) according to manufacturer's instructions and using E. coli XL-2 Blue cells
15 supercompetent cells or methylation-deficient SCS110 cells (in case of the methylation sensitive restriction enzymes XbaI or ClaI; both cell types available from Stratagene, La Jolla, CA). Desired regions from this PCR fragment were then cut out of the vectors using the abovementioned site-specific restriction enzymes. These fragments were joined in consecutive steps by subcloning into a pGEM[®]-T Easy vector. Finally, the
20 complete gene fragment was subcloned into pcDNA3.1⁺, under the CMV promoter. This provides a construct ready for transfection into any cell type for the purposes of determining the effect of overexpression of TRAG, for example, in RLE phi 13 cells, which normally have low levels of this protein (as demonstrated in Examples 1 and 4).

25

EXAMPLE 9

Generation of TRAG Transgenic and Knockout Mice

To elucidate more fully the potential role of TRAG in development and in carcinogenesis, the breeding of a knockout mouse is carried out. Part of the TRAG gene is deleted from a mouse line by standard knockout techniques, resulting in a truncated or
30 nonexistent protein product (as described above in section D.3). If the complete removal of the TRAG gene product produces an embryonic lethal, a conditional knockout could be considered. This involves engineering the TRAG knockout construct in such a way

that the deletion of the critical region of the TRAG gene occurs only after embryogenesis. In this way, the role of TRAG in an adult animal can be examined.

To determine the role of TRAG in an aggressive phenotype in tumor cell lines, a transgenic mouse model can be studied. To study a transgenic mouse model, the TRAG gene is inserted into the mouse genome under the control of a strong, constitutively active promoter element (which causes large amounts of the protein to be made at all times) or a conditionally active promoter element (which would induce large amounts of TRAG only on a specific stimulus). (See, for example, C Jhappen et al., *Cell*, 61:1137 (1990)). TRAG overexpression is evaluated by Northern blot analysis, as described in Example 1. In particular, the transgenic mice are studied to determine if TRAG overexpression shows more rapid or enhanced tumor formation or more aggressive metastasis.

TABLES

Table 1 shows the cDNA (SEQ ID NO: 1) and amino acid (SEQ ID NO: 2) sequences of rat TRAG from liver as determined by double strand sequence analysis of PCR products amplified from RLE (rat liver epithelium) cell and Fisher F344 rat brain tissue cDNA. The WD repeat elements are indicated by the underline, and the two tyrosine phosphorylation motifs are indicated in boldface type.

20	10	20	30	40	50
	GAAGCTTTGACAGGTTTGAAAAACACAATGGCAGGAAACAGTCTAGTTCTGCCATT				
					MetAlaGlyAsnSerLeuValLeuProIle
25	60	70	80	90	100
	GTTCTCTGGGGCCGCAAGCACCCACACACTGTATTTCGTCAATACTGCTGACAGAT				
	ValLeuTrpGlyArgLysAlaProThrHisCysIleSerSerIleLeuLeuThrAsp				
30	120	130	140	150	160
	GATGGGGGCACGATTGTGACTGGATGCCACGATGGACAGATATGTCTCTGGGATCTC				
	AspGlyGlyThrIleValThrGlyCysHisAspGlyGlnIleCysLeuTrpAspLeu				
35	180	190	200	210	220
	TCAGAAGAGCTGGAAGTTAATCCCCGAGCACTATTATTGGTCACACAGCAGCCATC				
	SerGluGluLeuGluValAsnProArgAlaLeuLeuPheGlyHisThrAlaAlaIle				
40	230	240	250	260	270
	ACTTGTTTGTCAAAAGCCTGTGCTTCTGGAGACAAACAGTACACCGTGAGTGCGTCC				
	ThrCysLeuSerLysAlaCysAlaSerGlyAspLysGlnTyrThrValSerAlaSer				
	290	300	310	320	330
	GCAAATGGAGAGATGTGCCTCTGGGATGTGAATGACGGCAGATGTATTGAATTTACA				
	AlaAsnGlyGluMetCysLeuTrpAspValAsnAspGlyArgCysIleGluPheThr				
	350	360	370	380	390

AAATTAGCCTGCACACATACTGGCATAACAGTTCTACCAGTTCTCTGTTGGAAATCAG
 LysLeuAlaCysThrHisThrGlyIleGlnPheTyrGlnPheSerValGlyAsnGln

400 410 420 430 440 450
 5 CGAGAGGGAAGGCTTCTGTGCCATGGGCATTACCCCTGAAATCCTCGTTGTGGATGCC
 ArgGluGlyArgLeuLeuCysHisGlyHisTyrProGluIleLeuValValAspAla

460 470 480 490 500 510
 10 ACCAGCCTTGAGGTGTTGTATTCCTTGGTATCGAAGATCTCTCCAGACTGGATCAGC
 ThrSerLeuGluValLeuTyrSerLeuValSerLysIleSerProAspTrpIleSer

520 530 540 550 560 570
 15 TCCATGAGYATYATCCGCTCTCACCGGACACAAGAGGACACTGTGGTAGCGCTGTCC
 SerMetSerIleIleArgSerHisArgThrGlnGluAspThrValValAlaLeuSer

580 590 600 610 620
 20 GTGACAGGTATTCTGAAGGTGTGGATTGTGACCTCTGAAATTAGTGGATTGCAGGAC
 ValThrGlyIleLeuLysValTrpIleValThrSerGluIleSerGlyLeuGlnAsp

630 640 650 660 670 680
 25 ACTGAGCCAATATTTGAGGAGGAATCCAAACCAATTTATTGTGAGAATTGCCAAAGC
 ThrGluProIlePheGluGluSerLysProIleTyrCysGlnAsnCysGlnSer

690 700 710 720 730 740
 30 CTCTCTTTTGTGCATTACACAGAGGTCGCTCTTGGTTGTATGCTCCAAGTACTGG
 LeuSerPheCysAlaPheThrGlnArgSerLeuLeuValValCysSerLysTyrTrp

750 760 770 780 790
 35 AGGGTGTTCGATGCTGGCGACTACTCCCTGCTGTGTTCAGGTCCTAGTGAAGATGGA
 ArgValPheAspAlaGlyAspTyrSerLeuLeuCysSerGlyProSerGluAspGly

800 810 820 830 840 850
 40 CAGACATGGACTGGAGGGGACTTTGTGTCTGCAGACAAAGTCATTATTTGGACTGAA
 GlnThrTrpThrGlyGlyAspPheValSerAlaAspLysValIleIleTrpThrGlu

860 870 880 890 900 910
 45 AACGGGCAGAGTTACATTTACAAACTCCCTGCCAGTTGCCTTCCAGCTAGTGATTCA
 AsnGlyGlnSerTyrIleTyrLysLeuProAlaSerCysLeuProAlaSerAspSer

920 930 940 950 960
 50 TTCCGCAGTGACGTGGGGAAGCAGTTGAAAATCTGATTCCCTCCCGTGCAGCATAGC
 PheArgSerAspValGlyLysAlaValGluAsnLeuIleProProValGlnHisSer

970 980 990 1000 1010 1020
 55 CTCTTGGATCAGAAGGATAGAGAGTTGGTAATTTGTCCTCCTGTTACTCGGTTTTTC
 LeuLeuAspGlnLysAspArgGluLeuValIleCysProProValThrArgPhePhe

1030 1040 1050 1060 1070 1080
 60 TATGGATGCAAGGAATATTTGCATAAGCTACTAATTCAGGGTGATTCTTCTGGAAGG
 TyrGlyCysLysGluTyrLeuHisLysLeuLeuIleGlnGlyAspSerSerGlyArg

1090 1100 1110 1120 1130 1140
 65 TTAAGTATTTGGAACATAGCAGACATAGCAGACAAACAGGAAGCCAATGAAGGGCTA
 LeuSerIleTrpAsnIleAlaAspIleAlaAspLysGlnGluAlaAsnGluGlyLeu

1150 1160 1170 1180 1190
 70 AAAACGACAACTTGATTAGTTTGCAAGATGCATTTGACAACTGAAGCCTTGTCTCT
 LysThrThrThrCysIleSerLeuGlnAspAlaPheAspLysLeuLysProCysPro

1200 1210 1220 1230 1240 1250
 75 GCTGGAATTATCGATCAGCTGAGTGTGATTCCAAACAGCAACGAACCACTTAAAGTA
 AlaGlyIleIleAspGlnLeuSerValIleProAsnSerAsnGluProLeuLysVal

1260 1270 1280 1290 1300 1310
 ACTGCGAGTGTCTACATACCAGCACACGGGCGCCTTGTTCGCGGCCGGGAAGACGGA
 ThrAlaSerValTyrIleProAlaHisGlyArgLeuValCysGlyArgGluAspGly
 5 1320 1330 1340 1350 1360
 AGCATCATTATCGTCCCTGCCACCCAGACGGCCATAGTTCAGCTGCTGCAGGGAGAA
 SerIleIleIleValProAlaThrGlnThrAlaIleValGlnLeuLeuGlnGlyGlu
 10 1370 1380 1390 1400 1410 1420
 CACATGCTCAGACGAGGTTGGCCCCGCACAGAACCTCCGTGGCCACCGGAACAAA
HisMetLeuArgArgGlyTrpProProHisArgThrLeuArgGlyHisArgAsnLys
 15 1430 1440 1450 1460 1470 1480
GTCACGTGTTTGCTGTATCCTCATCAGGTCTCAGCTCGGTATGATCAAAGATACCTG
ValThrCysLeuLeuTyrProHisGlnValSerAlaArgTyrAspGlnArgTyrLeu
 20 1490 1500 1510 1520 1530
ATATCCGGAGGTGTGGATTTTCCGTTCATCATTTGGGACATTTTCCGGAGAAATG
IleSerGlyGlyValAspPheSerValIleIleTrpAspIlePheSerGlyGluMet
 1540 1550 1560 1570 1580 1590
 AAACATATCTTCTGTGTTCATGGTGGTGAGATCACACAACCTCTGGTCCCGCCAGAA
 LysHisIlePheCysValHisGlyGlyGluIleThrGlnLeuLeuValProProGlu
 25 1600 1610 1620 1630 1640 1650
 AACTGTAGTGCAAGAGTTCAACACTGCGTCTGTTCTGTGGCCAGTGACCCTCTGTA
 AsnCysSerAlaArgValGlnHisCysValCysSerValAlaSerAspHisSerVal
 30 1660 1670 1680 1690 1700 1710
 GGGCTGCTAAGCTGCGAGAGAAAAATGCATCATGCTGGCGTCTCGTCCACCTGTTTC
GlyLeuLeuSerLeuArgGluLysLysCysIleMetLeuAlaSerArgHisLeuPhe
 35 1720 1730 1740 1750 1760
CCTATTACAGGTGATCAAGTGGAGGCCTTCTGACGACTACCTGGTGGTGGGGTGACG
ProIleGlnValIleLysTrpArgProSerAspAspTyrLeuValValGlyCysThr
 40 1770 1780 / 1790 1800 1810 1820
GACGGCTCTGTGTGTCTGGCAGATGGACACTGGTGCGCTGGACCGCTGTGCAATG
AspGlySerValCysValTrpGlnMetAspThrGlyAlaLeuAspArgCysAlaMet
 1830 1840 1850 1860 1870 1880
 GGGATAACAGCCGTGGAGATTCTCAATGCTTGTGACGAAGCTGTCCCTGCAGCAGTG
 GlyIleThrAlaValGluIleLeuAsnAlaCysAspGluAlaValProAlaAlaVal
 45 1890 1900 1910 1920 1930
 GACTCACTCAGTCACCCAGCAGTCAACCTGAAGCAAGCCATGACACGGCGGAGTCTC
 AspSerLeuSerHisProAlaValAsnLeuLysGlnAlaMetThrArgArgSerLeu
 50 1940 1950 1960 1970 1980 1990
 GCCGCCCTTAAAAACATGGCCCAACCAAGCTGCAAACCTTGCAACTAACCTTTTG
 AlaAlaLeuLysAsnMetAlaHisHisLysLeuGlnThrLeuAlaThrAsnLeuLeu
 55 2000 2010 2020 2030 2040 2050
 GCTTCTGAGGCCTCTGACAAGGGGAATTACCTAAATATTCTCATAACTCCCTGTATG
 AlaSerGluAlaSerAspLysGlyAsnLeuProLysTyrSerHisAsnSerLeuMet
 60 2060 2070 2080 2090 2100
 GTTCAAGCAATAAAGACAAACCTAACTGACCCGATATCCATGTGCTTTTCTTTGAT
 ValGlnAlaIleLysThrAsnLeuThrAspProAspIleHisValLeuPhePheAsp
 2110 2120 2130 2140 2150 2160
 GTGGAAGCTTTGATTATTCAACTCCTGACTGAAGAAGCCTCTAGGCCGAATACTGCA
 ValGluAlaLeuIleIleGlnLeuLeuThrGluGluAlaSerArgProAsnThrAla

2170 2180 2190 2200 2210 2220
CTTATTTCCCAGAGAATCTGCAGAAAGCATCTGGCAGTTCAGACAAGGGGGCTCT
LeuIleSerProGluAsnLeuGlnLysAlaSerGlySerSerAspLysGlyGlySer
5
2230 2240 2250 2260 2270 2280
TTCCTGACTGGAAAACGAGCGGCAGTCTTTTCCAGCAAGTGAAGAACTATCAAA
PheLeuThrGlyLysArgAlaAlaValLeuPheGlnGlnValLysGluThrIleLys
10
2290 2300 2310 2320 2330
GAGAACATAAAGGAGCACCTCCTTGATGAGGAGGAGGACGAGGAAGAGGTGATGAGG
GluAsnIleLysLysGluHisLeuLeuAspGluGluGluAspGluGluValMetArg
15
2340 2350 2360 2370 2380 2390
CAGAGGAGGGAAGAAAGTGACCCCTGAGTACCGGGCCAGCAAGTCCAAACCACTTACC
GlnArgArgGluGluSerAspProGluTyrArgAlaSerLysSerLysProLeuThr
20
2400 2410 2420 2430 2440 2450
CTACTAGAATACACCTTACTATGGATACCGCAAAATTATTATGTCTGTCTCCAC
LeuLeuGluTyrAsnLeuThrMetAspThrAlaLysLeuPheMetSerCysLeuHis
25
2460 2470 2480 2490 2500
GCCTGGGGTTTGAATGAAGTTCTGGATGAAGTTGCCTCGATCGCCTCGGCATGCTG
AlaTrpGlyLeuAsnGluValLeuAspGluValCysLeuAspArgLeuGlyMetLeu
2510 2520 2530 2540 2550 2560
AAACCACACTGCACAGTGTCTTGGTCTCCTATCCAGAGGAGGTCTATATGTCCTTG
LysProHisCysThrValSerPheGlyLeuLeuSerArgGlyGlyHisMetSerLeu
30
2570 2580 2590 2600 2610 2620
ATGCTTCCTGGTTATAATCAGGCTGCTGGAAAGCTACTGCAGGCGAAAGCAGAAGCA
MetLeuProGlyTyrAsnGlnAlaAlaGlyLysLeuLeuGlnAlaLysAlaGluAla
35
2630 2640 2650 2660 2670
GGACGGAAGGGGCCAGCAACGGAGAGCGTAGGCAAGGGGACCTACACAGTGTCCCGA
GlyArgLysGlyProAlaThrGluSerValGlyLysGlyThrTyrThrValSerArg
2680 2690 2700 2710 2720 2730
GCGGTCACCACGCAACATCTGTGTCCATCATATCTCTGGCAAATACTTTAATGAGC
AlaValThrThrGlnHisLeuLeuSerIleIleSerLeuAlaAsnThrLeuMetSer
40
2740 2750 2760 2770 2780 2790
ATGACCAATGCGACGTTCATTGGAGATCACATGAAGAAGGGCCCCACAGGCCGCCT
MetThrAsnAlaThrPheIleGlyAspHisMetLysLysGlyProThrArgProPro
45
2800 2810 2820 2830 2840 2850
AGACCAGGCACCCAGACCTTTCTAAGGCAAGGGATTCCCCCAGCCTCCAGTAAC
ArgProGlyThrProAspLeuSerLysAlaArgAspSerProProAlaSerSerAsn
50
2860 2870 2880 2890 2900
ATTGTGCAAGGACAGATTAAACAAGCTGCTGCGCCTGTCTCTGCTCGGTCTGCCGCC
IleValGlnGlyGlnIleLysGlnAlaAlaAlaProValSerAlaArgSerAlaAla
55
2910 2920 2930 2940 2950 2960
GACCACTCTGGCTCTGCCTCTGCTTACGTACCTGCTTCTTAGTGAAT
AspHisSerGlySerAlaSerAlaSerProAlaLeuArgThrCysPheLeuValAsn
60
2970 2980 2990 3000 3010 3020
GAAGGATGGAGCCAACTAGCTGCCATGCACTGTGTCTGCTGCCGACCTGCTGGGG
GluGlyTrpSerGlnLeuAlaAlaMetHisCysValMetLeuProAspLeuLeuGly
3030 3040 3050 3060 3070
CTGGGTAAATTACAGGCCTCCTCTCTGGAGATGCTAGCTCGAAGATGGCAAGATCGG

LeuGlyLysPheArgProProLeuLeuGluMetLeuAlaArgArgTrpGlnAspArg

3080 3090 3100 3110 3120 3130
5 TGCTTGGAGGTGAGAGAGGCTGCACAGGCCCTTCTTCTAGCAGAGCTGAGAAGAATT
CysLeuGluValArgGluAlaAlaGlnAlaLeuLeuLeuAlaGluLeuArgArgIle

3140 3150 3160 3170 3180 3190
10 GAGCAGGCAGGACGGAAGGAGACTATTGATACCTGGGCTCCTTACCTACCTCAGTAC
GluGlnAlaGlyArgLysGluThrIleAspThrTrpAlaProTyrLeuProGlnTyr

3200 3210 3220 3230 3240
15 ATGGACCATGTCATATCACCTGGAGTCACGGCGGAAGCCATGCAGACTATGGCAGCT
MetAspHisValIleSerProGlyValThrAlaGluAlaMetGlnThrMetAlaAla

3250 3260 3270 3280 3290 3300
20 GCTCCAGATGCCTCGGGGCCAGAAGCCAAAGTCCAGGAAGAAGAGCATGACCTCGTG
AlaProAspAlaSerGlyProGluAlaLysValGlnGluGluGluHisAspLeuVal

3310 3320 3330 3340 3350 3360
25 GACGATGACATCACTGCTTATCAAGTGTCCACAAATGAAAAGATGTCC
AspAspAspIleThrThrGlyCysLeuSerSerValProGlnMetLysLysMetSer

3370 3380 3390 3400 3410 3420
30 ACATCTTACGAAGAAAGAAGGAAGCAGGCCACTGCTATTGTTCTCTGGGAGTGATA
ThrSerTyrGluGluArgArgLysGlnAlaThrAlaIleValLeuLeuGlyValIle

3430 3440 3450 3460 3470
35 GGAGCAGAGTTTGGAGCTGAAATTGAACCACCAAACCTGCTGACCAGACCTCGGAGC
GlyAlaGluPheGlyAlaGluIleGluProProLysLeuLeuThrArgProArgSer

3480 3490 3500 3510 3520 3530
40 TCTAGTCAAATTCCTGAAGGATTGGTTTGACAAGTGGAGGTTCCAACTACTCTCTG
SerSerGlnIleProGluGlyPheGlyLeuThrSerGlyGlySerAsnTyrSerLeu

3540 3550 3560 3570 3580 3590
45 GCCAGACATACGTGCAAGGCACTGACATTTCTCTGCTACAGCCACCAAGTCCCAA
AlaArgHisThrCysLysAlaLeuThrPheLeuLeuLeuGlnProProSerProLys

3600 3610 3620 3630 3640
50 CTTCTCTCATAGCACCATCCGGAGAACTGCCATTGACCTGATCGGGCGAGGGTTC
LeuProProHisSerThrIleArgArgThrAlaIleAspLeuIleGlyArgGlyPhe

3650 3660 3670 3680 3690 3700
55 ACCGTGTGGGAGCCTTACATGGACGTGTCTGCTGCTGCTGATGGGGCTGCTGGAGCTG
ThrValTrpGluProTyrMetAspValSerAlaValLeuMetGlyLeuLeuGluLeu

3710 3720 3730 3740 3750 3760
60 TGTGCAGATGCTGAGAAGCAGCTGGCCAACATCACAAATGGGGCTGCCTCTGAGCCCT
CysAlaAspAlaGluLysGlnLeuAlaAsnIleThrMetGlyLeuProLeuSerPro

3770 3780 3790 3800 3810
GCAGCTGACTCTGCCGATCCGCAAGACACGCCCTTCTCTCATAGCCACCGCCAGA
AlaAlaAspSerAlaArgSerAlaArgHisAlaLeuSerLeuIleAlaThrAlaArg

3820 3830 3840 3850 3860 3870
65 CCACCCGCCTTCATCACCACCATAGCTAAGGAGGTGCACAGACACAGGCCCTTGCA
ProProAlaPheIleThrThrIleAlaLysGluValHisArgHisThrAlaLeuAla

3880 3890 3900 3910 3920 3930
70 GCAAATACCCAGTCCCAGCAGATATCCACACCACCACTGGCAAGGGCTAAAGGC
AlaAsnThrGlnSerGlnGlnSerIleHisThrThrThrLeuAlaArgAlaLysGly

3940 3950 3960 3970 3980 3990

GAAATCCTGAGAGTCATTGAAATTCCTATCGAAAAGATGCCTACGGATGTTGTGGAT
 GluIleLeuArgValIleGluIleLeuIleGluLysMetProThrAspValValAsp

4000 4010 4020 4030 4040
 CTTCTTGTGGAGTCATGGACATCATCATGTACTGCCTGGAAGGATCTTTAGTTAAG
 LeuLeuValGluValMetAspIleIleMetTyrCysLeuGluGlySerLeuValLys

4050 4060 4070 4080 4090 4100
 AAGAAGGGTCTTCAGGAGTGTTCCTCCAGCCATCTGCAGGTTCTACATGGTCAGCTAT
 LysLysGlyLeuGlnGluCysPheProAlaIleCysArgPheTyrMetValSerTyr

4110 4120 4130 4140 4150 4160
 TATGAGCGGAGTCACAGAATTGCAGTTGGAGCACGCCATGGCTCAGTGGCCCTGTAT
 TyrGluArgSerHisArgIleAlaValGlyAlaArgHisGlySerValAlaLeuTyr

4170 4180 4190 4200 4210
 GACATCCGGACTGGGAAATGTCTAGACAATCCACGGACACAAGGGACCTATCACTGCA
 AspIleArgThrGlyLysCysGlnThrIleHisGlyHisLysGlyProIleThrAla

4220 4230 4240 4250 4260 4270
 GTGTCCTTTGCTCCTGATGGGCGTTACCTTGCCACCTACTCAAACACTGACAGCCAC
 ValSerPheAlaProAspGlyArgTyrLeuAlaThrTyrSerAsnThrAspSerHis

4280 4290 4300 4310 4320 4330
 ATTTCTTTCTGGCAGATGAACACCTCACTTCTGGGAAGCATTGGCATGCTGAAGTCA
 IleSerPheTrpGlnMetAsnThrSerLeuLeuGlySerIleGlyMetLeuAsnSer

4340 4350 4360 4370 4380
 GCACCTCAGCTGCGCTGCATCAAGACCTACCAGGTACCTCCAGTGCAGCCCGCATCC
 AlaProGlnLeuArgCysIleLysThrTyrGlnValProProValGlnProAlaSer

4390 4400 4410 4420 4430 4440
 CCTGGCTCGCACAAACGCCCTCAGGTTGGCCCGGCTCATCTGGACTTCCAACCGGAAT
 ProGlySerHisAsnAlaLeuArgLeuAlaArgLeuIleTrpThrSerAsnArgAsn

4450 4460 4470 4480 4490
 GTTATCCTCATGGCCACGATGGGAAGGAGCACCGCTTCATGGTCTGA
 ValIleLeuMetAlaHisAspGlyLysGluHisArgPheMetValSTP

Table 2 shows the cDNA (SEQ ID NO: 3) and amino acid (SEQ ID NO: 4) sequences of human TRAG from brain as determined by double strand sequence of PCR products amplified from human liver tissue cDNA. The WD repeat elements are indicated by the underline, and the two tyrosine phosphorylation motifs are indicated in boldface type.

10 20 30 40 50
 TAACATGTTTTCGAGAGAAATATTGTAATATCTGACAAATTTTATAACATTTTCAGG

60 70 80 90 100 110
 TTTGAAAACACAAACACAATGGCAGGAAACAGCCTTGTCTACCCATTGTTCTTTGG
 MetAlaGlyAsnSerLeuValLeuProIleValLeuTrp

120 130 140 150 160 170
 GGTCGAAAAGCGCCACACATTGCATCTCAGCCGTACTTTTAAACAGATGATGGGGCC
 GlyArgLysAlaProThrHisCysIleSerAlaValLeuLeuThrAspAspGlyAla

180 190 200 210 220
 ACGATCGTAACAGGATGTCACGACGGACAAATATGTCTCTGGGATCTTTCAGTAGAA
 ThrIleValThrGlyCysHisAspGlyGlnIleCysLeuTrpAspLeuSerValGlu

230 240 250 260 270 280
CTGCAAGTTAATCCTCGAGCACTGTTGTTTGGTCATACAGCATCAATCACTTGTGTTG
LeuGlnValAsnProArgAlaLeuLeuPheGlyHisThrAlaSerIleThrCysLeu

5 290 300 310 320 330 340
TCTAAAGCTTGTGCTTCCAGTGACAAACAGTATATTGTGAGTGCATCTGAAAGTGGA
SerLysAlaCysAlaSerSerAspLysGlnTyrIleValSerAlaSerGluSerGly

10 350 360 370 380 390
GAGATGTGCCTCTGGGATGTGAGTGTGGCAGATGTATTGAATTTACAAAATTAGCT
GluMetCysLeuTrpAspValSerAspGlyArgCysIleGluPheThrLysLeuAla

15 400 410 420 430 440 450
TGACACATACTGGCATACTACAGTTCTACCAGTTCTCTGTTGGGAATCAGCGAGAAGGA
CysThrHisThrGlyIleGlnPheTyrGlnPheSerValGlyAsnGlnArgGluGly

20 460 470 480 490 500 510
AGGCTTTTATGCCACGGACATTACCCTGAAATCCTTGTGTGGATGCTACCAGCCTT
ArgLeuLeuCysHisGlyHisTyrProGluIleLeuValValAspAlaThrSerLeu

25 520 530 540 550 560 570
GAAGTATTATACTCCTTAGTATCAAAGATATCACCAGACTGGATTAGCTCCATGAGT
GluValLeuTyrSerLeuValSerLysIleSerProAspTrpIleSerSerMetSer

30 580 590 600 610 620
ATTATTCGATCCACCGAACACAAAGAGGACACAGTGGTAGCACTCTCGGTGACTGGC
IleIleArgSerHisArgThrGlnGluAspThrValValAlaLeuSerValThrGly

35 630 640 650 660 670 680
ATCCTGAAGGTCTGGATTGTTACCTCGGAAATAAGTGACATGCAGGATACTGAGCCA
IleLeuLysValTrpIleValThrSerGluIleSerAspMetGlnAspThrGluPro

40 690 700 710 720 730 740
ATATTTGAGGAGGAATCCAAACCAATTTATTGTCAGAATTGCCAAAGCATCTCTTTT
IlePheGluGluGluSerLysProIleTyrCysGlnAsnCysGlnSerIleSerPhe

45 750 760 770 780 790
TGTGCATTACACAAAGGTCACCTTTGGTTGTGTGTTCCAAATATTGGAGGGTGTTC
CysAlaPheThrGlnArgSerLeuLeuValValCysSerLysTyrTrpArgValPhe

50 800 810 820 830 840 850
GATGCCGGAGACTATTCCTTGTGTGTTTCAGGTCTAGTGAAAATGGACAGACATGG
AspAlaGlyAspTyrSerLeuLeuCysSerGlyProSerGluAsnGlyGlnThrTrp

55 860 870 880 890 900 910
ACCGGGGGGACTTTGTCTCATCAGATAAAGTCATCATTTGGACAGAAAATGGGCAA
ThrGlyGlyAspPheValSerSerAspLysValIleIleTrpThrGluAsnGlyGln

60 920 930 940 950 960
AGTTATATTTACAACTACCTGCCAGTTGCCTTCCAGCTAGTGATTTCATCCGCAGT
SerTyrIleTyrLysLeuProAlaSerCysLeuProAlaSerAspSerPheArgSer

970 980 990 1000 1010 1020
GATGTGGGGAAGGCAGTTGAAAATTTAATTCCTCCTGTACAACATATCCTCTTGGAT
AspValGlyLysAlaValGluAsnLeuIleProProValGlnHisIleLeuLeuAsp

1030 1040 1050 1060 1070 1080
CGAAAAGATAAAGAGTTGCTAATTTGTCCTCCTGTTACTCGGTTCTTCTATGGATGC
ArgLysAspLysGluLeuLeuIleCysProProValThrArgPhePheTyrGlyCys

1090 1100 1110 1120 1130 1140
AGAGAATATTTCCATAAACTGTTAATTACGGGTGATTCTTCTGGAAGGTTGAATATT

ArgGluTyrPheHisLysLeuLeuIleGlnGlyAspSerSerGlyArgLeuAsnIle

1150 1160 1170 1180 1190
 TGGAAACATATCAGACACAGCTGATAAACAGGGAAGTGAAGAAGGGCTGGCAATGACA
 5 TrpAsnIleSerAspThrAlaAspLysGlnGlySerGluGluGlyLeuAlaMetThr

1200 1210 1220 1230 1240 1250
 ACTTCTATTAGTTTGAAGAGGCATTTGATAAACTGAATCCTTGTCCTGCTGGAATT
 10 ThrSerIleSerLeuGlnGluAlaPheAspLysLeuAsnProCysProAlaGlyIle

1260 1270 1280 1290 1300 1310
 ATAGATCAGCTGAGTGTGATTCCCAATAGTAATGAACCTCTTAAAGTAACTGCAAGT
 IleAspGlnLeuSerValIleProAsnSerAsnGluProLeuLysValThrAlaSer

1320 1330 1340 1350 1360
 GTGTACATACCAGCACATGGACGACTTTTGTGGTCGTGAAGATGGAAGCATAGTT
 15 ValTyrIleProAlaHisGlyArgLeuValCysGlyArgGluAspGlySerIleVal

1370 1380 1390 1400 1410 1420
 ATTGTACCTGCCACACAGACGGCCATAGTACAGCTGTTGCAAGGGGAACACATGCTC
 20 IleValProAlaThrGlnThrAlaIleValGlnLeuLeuGlnGlyGluHisMetLeu

1430 1440 1450 1460 1470 1480
 AGAAGAGGTTGGCCACCTCACAGAACACTCCGTGGTCATCGGAACAAAGTCACATGT
 25 ArgArgGlyTrpProProHisArgThrLeuArgGlyHisArgAsnLysValThrCys

1490 1500 1510 1520 1530
 TTGCTATATCCTCATCAGGTCTCAGCTCGGTATGATCAAAGATACCTGATATCTGGA
 30 LeuLeuTyrProHisGlnValSerAlaArgTyrAspGlnArgTyrLeuIleSerGly

1540 1550 1560 1570 1580 1590
 GGTGTGGATTTTTCAGTCATAATTGGGACATATTTCTGGAGAAATGAAACATATC
 GlyValAspPheSerValIleIleTrpAspIlePheSerGlyGluMetLysHisIle

1600 1610 1620 1630 1640 1650
 TTCTGTGTTTCATGGTGGTGAGATTACTCAACTTCTAGTTCCACCTGAAAACGTAGT
 35 PheCysValHisGlyGlyGluIleThrGlnLeuLeuValProProGluAsnCysSer

1660 1670 1680 1690 1700 1710
 GCAAGAGTACAGCACTGCATCTGCTCTGTAGCCAGTGACCCTCAGTAGGACTTCTA
 40 AlaArgValGlnHisCysIleCysSerValAlaSerAspHisSerValGlyLeuLeu

1720 1730 1740 1750 1760
 AGTTTGCAGAGAAAAATGCATAATGTTGGCATCTCGTCACCTTTTTCCTATTCAA
 45 SerLeuArgGluLysLysCysIleMetLeuAlaSerArgHisLeuPheProIleGln

1770 1780 1790 1800 1810 1820
 GTAATCAAATGGAGGCCTTCTGATGATTACCTGGTGGTGGGTGTTTCAGATGGTTCT
 50 ValIleLysTrpArgProSerAspAspTyrLeuValValGlyCysSerAspGlySer

1830 1840 1850 1860 1870 1880
 GTGTACGTCTGGCAAATGGATACTGGTGCATTGGATCGTTGTGTGATGGGGATAACA
 ValTyrValTrpGlnMetAspThrGlyAlaLeuAspArgCysValMetGlyIleThr

1890 1900 1910 1920 1930
 GCAGTTGAGATTCTAAACGCTTGTGATGAAGCTGTTCTGCTGCTGTTGATTCACTT
 55 AlaValGluIleLeuAsnAlaCysAspGluAlaValProAlaAlaValAspSerLeu

1940 1950 1960 1970 1980 1990
 AGTCATCCAGCAGTCAACCTAAAACAAGCTATGACGAGACGTAGTCTTGCTGCTCTT
 60 SerHisProAlaValAsnLeuLysGlnAlaMetThrArgArgSerLeuAlaAlaLeu

2000 2010 2020 2030 2040 2050

AAAAATATGGCCCATCATAAGCTACAAACCCTTGCAACTAACCTCTTGGCTTCTGAG
LysAsnMetAlaHisHisLysLeuGlnThrLeuAlaThrAsnLeuLeuAlaSerGlu

2060 2070 2080 2090 2100
5 GCATCTGACAAGGGAAATTTACCTAAATATTCTCATAACTCCCTGATGGTTCAAGCA
AlaSerAspLysGlyAsnLeuProLysTyrSerHisAsnSerLeuMetValGlnAla

2110 2120 2130 2140 2150 2160
10 ATAAAGACAAACCTAACAGACCCGGACATACATGTGCTATTCTTTGATGTGGAAGCG
IleLysThrAsnLeuThrAspProAspIleHisValLeuPhePheAspValGluAla

2170 2180 2190 2200 2210 2220
15 TTGATTATTCACTCCTGACTGAAGAAGCCTCTAGGCCGAATACTGCTCTTATTTCC
LeuIleIleGlnLeuLeuThrGluGluAlaSerArgProAsnThrAlaLeuIleSer

2230 2240 2250 2260 2270 2280
20 CCAGAGATTTGCAAAAAGCATCTGGCAGTTCAGACAAAGGGGCTCTTTTAACT
ProGluAsnLeuGlnLysAlaSerGlySerSerAspLysGlyGlySerPheLeuThr

2290 2300 2310 2320 2330
25 GGAAAACGAGCAGCAGTTCTCTTCCAAACAGTGAAGAAACGATCAAGAGAACATC
GlyLysArgAlaAlaValLeuPheGlnGlnValLysGluThrIleLysGluAsnIle

2340 2350 2360 2370 2380 2390
25 AAGGAACACCTCCTTGATGATGAAGAGGAGGATGAGGAGATAATGAGGCAGAGAAGG
LysGluHisLeuLeuAspAspGluGluGluAspGluGluIleMetArgGlnArgArg

2400 2410 2420 2430 2440 2450
30 GAAGAAAGTGATCCTGAATATCGGTCCAGCAAATCAAAGCCATTGACCCTATTAGAA
GluGluSerAspProGluTyrArgSerSerLysSerLysProLeuThrLeuLeuGlu

2460 2470 2480 2490 2500
35 TATAATTTAACTATGGACACTGCAAAGCTGTTTATGTCCTGCCTTCACGCCTGGGGT
TyrAsnLeuThrMetAspThrAlaLysLeuPheMetSerCysLeuHisAlaTrpGly

2510 2520 2530 2540 2550 2560
40 TTGAATGAAGTACTGGATGAAGTTTGCCTGGATCGCCTTGGAAATGTGAAACCCAC
LeuAsnGluValLeuAspGluValCysLeuAspArgLeuGlyMetLeuLysProHis

2570 2580 2590 2600 2610 2620
45 TGCACCGTATCGTTTGGCCTCTTGTCAAGAGGAGGCCATATGTCATGATGCTGCCG
CysThrValSerPheGlyLeuLeuSerArgGlyGlyHisMetSerLeuMetLeuPro

2630 2640 2650 2660 2670
45 GGTATAATCAGCCTGCTTGTAACCTGTCACATGGGAAAACAGAAGTAGGAAGGAAG
GlyTyrAsnGlnProAlaCysLysLeuSerHisGlyLysThrGluValGlyArgLys

2680 2690 2700 2710 2720 2730
50 CTGCCAGCGTCTGAGGGAGTAGGAAAGGGAACCTACGGAGTGTCCTGCGCTCACC
LeuProAlaSerGluGlyValGlyLysGlyThrTyrGlyValSerArgAlaValThr

2740 2750 2760 2770 2780 2790
55 ACACAGCATCTCCTGTCTATCATTTCTTTGGCAAATACTTTAATGAGTATGACCAAT
ThrGlnHisLeuLeuSerIleIleSerLeuAlaAsnThrLeuMetSerMetThrAsn

2800 2810 2820 2830 2840 2850
60 GCAACTTTTATTGGTGATCATATGAAGAAGGGTCCTACCAGGCCACCTAGACCAAGC
AlaThrPheIleGlyAspHisMetLysLysGlyProThrArgProProArgProSer

2860 2870 2880 2890 2900
60 ACCCCAGACCTTTCTAAGGCAAGGGGTCCCTCCAACTTCCAGTAATATTGTGCAA
ThrProAspLeuSerLysAlaArgGlySerProProThrSerSerAsnIleValGln

2910 2920 2930 2940 2950 2960
GGACAGATTAAACAAGTTGCTGCACCTGTCGTTTCCGCTCGGTCTGATGCTGATCAC
GlyGlnIleLysGlnValAlaAlaProValValSerAlaArgSerAspAlaAspHis

5 2970 2980 2990 3000 3010 3020
TCTGGCTCTGACCCTCCTTCTGCTCCTGCTTTACATACCTGTTTCTTAGTAAATGAA
SerGlySerAspProProSerAlaProAlaLeuHisThrCysPheLeuValAsnGlu

10 3030 3040 3050 3060 3070
GGTTGGAGTCAGTTAGCTGCTATGCACTGTGTTATGCTGCCAGACCTACTGGGATTG
GlyTrpSerGlnLeuAlaAlaMetHisCysValMetLeuProAspLeuLeuGlyLeu

15 3080 3090 3100 3110 3120 3130
GATAAATTTAGGCCTCCCTTCTGGAGATGTGCGCCGAAGATGGCAAGATCGATGC
AspLysPheArgProProLeuLeuGluMetLeuAlaArgArgTrpGlnAspArgCys

20 3140 3150 3160 3170 3180 3190
TTGGAGGTGAGAGAAGCCGCACAGGCCCTGCTTCTGGCGGAAGTGAAGAATTGAG
LeuGluValArgGluAlaAlaGlnAlaLeuLeuLeuAlaGluLeuArgArgIleGlu

25 3200 3210 3220 3230 3240
CAGGCAGGCAGGAAGGAAGCCATTGATGCCTGGGCTCCTTACTTACTCAGTACATA
GlnAlaGlyArgLysGluAlaIleAspAlaTrpAlaProTyrLeuProGlnTyrIle

3250 3260 3270 3280 3290 3300
GACCACGTCATATCACCTGGAGTCACATCAGAAGCCGCGCAGACTATCACCACGGCT
AspHisValIleSerProGlyValThrSerGluAlaAlaGlnThrIleThrThrAla

30 3310 3320 3330 3340 3350 3360
CCTGATGCCTCAGGGCCTGAAGCAAAAGTCCAGGAGGAAGAGCATGACCTTGTGAC
ProAspAlaSerGlyProGluAlaLysValGlnGluGluGluHisAspLeuValAsp

35 3370 3380 3390 3400 3410 3420
GATGACATCACCCTGGTTGCTTATCAAGTGTCCACAAATGAAAAAATTTCTACA
AspAspIleThrThrGlyCysLeuSerSerValProGlnMetLysLysIleSerThr

40 3430 3440 3450 3460 3470
TCTTACGAGGAAGACGGAAGCAAGCTACCGCTATTGTTTTACTTGGAGTAATAGGA
SerTyrGluGluArgArgLysGlnAlaThrAlaIleValLeuLeuGlyValIleGly

45 3480 3490 3500 3510 3520 3530
GCTGAATTTGGTGCTGAAATTGAACCTCCTAAACTATTGACCAGACCTCGAAGCTCT
AlaGluPheGlyAlaGluIleGluProProLysLeuLeuThrArgProArgSerSer

50 3540 3550 3560 3570 3580 3590
AGCCAAATTCCTGAGGGATTCGGGTTGACTAGTGGTGGATCCAACCTACTCGTGGCC
SerGlnIleProGluGlyPheGlyLeuThrSerGlyGlySerAsnTyrSerLeuAla

55 3600 3610 3620 3630 3640
AGACATACTTGCAAGGCACTGACGTTTCTTCTGCTACAGCCTCCAAGCCCCAACTT
ArgHisThrCysLysAlaLeuThrPheLeuLeuLeuGlnProProSerProLysLeu

60 3650 3660 3670 3680 3690 3700
CCTCCACACAGCACTATCCGAAGAAGCAGCCATTGATCTGATTGGACGTGGGTTCACT
ProProHisSerThrIleArgThrAlaIleAspLeuIleGlyArgGlyPheThr

3710 3720 3730 3740 3750 3760
GTTTGGGAGCCTTACATGGATGTGTCGCTGTTCTGATGGGGCTTCTCGAAGTTTGT
ValTrpGluProTyrMetAspValSerAlaValLeuMetGlyLeuLeuGluLeuCys

3770 3780 3790 3800 3810
GCCGATGCCGAGAAACAACCTTGCCAACATCACAATGGGGTTGCCTCTGAGCCCAGCA
AlaAspAlaGluLysGlnLeuAlaAsnIleThrMetGlyLeuProLeuSerProAla

```

3820      3830      3840      3850      3860      3870
GCTGACTCGGCCCGCTCTGCGAGGCATGCCCTCTCGCTCATTGCCACCGCCAGACCA
AlaAspSerAlaArgSerAlaArgHisAlaLeuSerLeuIleAlaThrAlaArgPro
5
      3880      3890      3900      3910      3920      3930
CCCGCCTTCATCACCACCATAGCCAAAGAGGTACACAGACATACGGCTCTTGCAGCA
ProAlaPheIleThrThrIleAlaLysGluValHisArgHisThrAlaLeuAlaAla
10
      3940      3950      3960      3970      3980      3990
AATACCCAATCACAGCAGAATATGCACACAACAACTCTGCACGAGCTAAAGGGGAA
AsnThrGlnSerGlnGlnAsnMetHisThrThrThrLeuAlaArgAlaLysGlyGlu
15
      4000      4010      4020      4030      4040
ATTTTGAGAGTCATTGAAATTCTTATTGAAAAGATGCCACAGATGTTGTGGATCTT
IleLeuArgValIleGluIleLeuIleGluLysMetProThrAspValValAspLeu
20
4050      4060      4070      4080      4090      4100
CTCGTGGAGGTTATGGACATCATTATGTACTGCCTTGAAGGATCTTTAGTTAAAAAG
LeuValGluValMetAspIleIleMetTyrCysLeuGluGlySerLeuValLysLys
25
      4110      4120      4130      4140      4150      4160
AAAGGTCTTCAAGAATGTTTCCAGCCATCTGCAGGTTCTACATGGTCAGCTATTAT
LysGlyLeuGlnGluCysPheProAlaIleCysArgPheTyrMetValSerTyrTyr
30
      4170      4180      4190      4200      4210
GAGCGGAATCACAGAATAGCAGTTGGAGCTCGCCATGGTTTCAGTGGCCCTGTACGAC
GluArgAsnHisArgIleAlaValGlyAlaArgHisGlySerValAlaLeuTyrAsp
35
4220      4230      4240      4250      4260      4270
ATCCGGACTGGAAATGTGACACAATCCATGGACACAAGGGACCAATCACTGCAGTG
IleArgThrGlyLysCysGlnThrIleHisGlyHisLysGlyProIleThrAlaVal
40
      4280      4290      4300      4310      4320      4330
GCTTTTGCTCCTGATGGAAGATATCTTGCCACCTACTCAAACACTGACAGCCACATT
AlaPheAlaProAspGlyArgTyrLeuAlaThrTyrSerAsnThrAspSerHisIle
45
      4340      4350      4360      4370      4380
TCTTTTGGCAGATGAACACGTCAGTCTGGGAAGCATCGGCATGCTGAACCTCGGCA
SerPheTrpGlnMetAsnThrSerLeuLeuGlySerIleGlyMetLeuAsnSerAla
50
4390      4400      4410      4420      4430      4440
CCTCAGCTGCGCTGCATTAAACCTACCAGGTGCCCCCTGTGCAGCCCGCGTCCCCC
ProGlnLeuArgCysIleLysThrTyrGlnValProProValGlnProAlaSerPro
55
      4450      4460      4470      4480      4490      4500
GGCTCCCACAATGCCCTCAAGCTGGCCCGGCTCATCTGGACTTCCAACCGCAACGTC
GlySerHisAsnAlaLeuLysLeuAlaArgLeuIleTrpThrSerAsnArgAsnVal
      4510      4520      4530      4540
ATCCTCATGGCCCATGACGGGAAGGAGCACCCTTCATGGTCTAA
IleLeuMetAlaHisAspGlyLysGluHisArgPheMetValSTP

```

Table 3 shows the cDNA (SEQ ID NO: 5) and amino acid (SEQ ID NO: 6) sequences of mouse TRAG from brain as determined by double strand sequence analysis of PCR products amplified from mouse liver and brain tissue cDNA. The WD repeat elements are indicated by the underline, and the two tyrosine phosphorylation motifs are indicated in boldface type.

10 20 30 40 50
TGAAGATTGACAGGTTTGAAAACGCCATGGCAGGAAACAGCCTAGTTCTGCCCATT
MetAlaGlyAsnSerLeuValLeuProIle

5 60 70 80 90 100 110
GTTCTTTGGGGCCGCAAAGCACCCACACATTGCATTTCGTCAATACTGTTGACAGAT
ValLeuTrpGlyArgLysAlaProThrHisCysIleSerSerIleLeuLeuThrAsp

10 120 130 140 150 160 170
GATGGGGGCACAATTGTAACGGATGCCACGATGGACAAATATGTCCTCTGGGATGTT
AspGlyGlyThrIleValThrGlyCysHisAspGlyGlnIleCysLeuTrpAspVal

15 180 190 200 210 220
TCGGTAGAACTAGAAGTTAATCCCCGAGCACTGTTATTGGCCACACAGCATCCATC
SerValGluLeuGluValAsnProArgAlaLeuLeuPheGlyHisThrAlaSerIle

20 230 240 250 260 270 280
ACTTGTGTTGTCAAAGCCTGCGCTTCTGGGGACAAGCGGTACACTGTGAGCGCGTCT
ThrCysLeuSerLysAlaCysAlaSerGlyAspLysArgTyrThrValSerAlaSer

25 290 300 310 320 330 340
GCAAACGGAGAGATGTGCCTCTGGGATGTGAACGATGGCAGATGTATTGAATTTACC
AlaAsnGlyGluMetCysLeuTrpAspValAsnAspGlyArgCysIleGluPheThr

30 350 360 370 380 390
AAGTTAGCCTGCACACACTGGCATACTTCTACCAGTTCTCTGTTGGGAACCAG
LysLeuAlaCysThrHisThrGlyIleGlnPheTyrGlnPheSerValGlyAsnGln

35 400 410 420 430 440 450
CAAGAGGGCAGGTCCTCTGCCATGGACATTACCCTGAAATCCTCGTTGTGGATGCC
GlnGluGlyArgLeuLeuCysHisGlyHisTyrProGluIleLeuValValAspAla

40 460 470 480 490 500 510
ACCAGCCTTGAGGTGTTGTATTCCTTGGTATCGAAGATCTCTCCAGACTGGATCAGC
ThrSerLeuGluValLeuTyrSerLeuValSerLysIleSerProAspTrpIleSer

45 520 530 540 550 560 570
TCCATGAGCATCATCCACTCTCAGCGGACACAAGAGGACACTGTGGTGGCGCTCTCT
SerMetSerIleIleHisSerGlnArgThrGlnGluAspThrValValAlaLeuSer

50 580 590 600 610 620
GTGACAGGTATTCTGAAGGTGTGGATTGTCACCTCTGAAATGAGTGAATGCAGGAT
ValThrGlyIleLeuLysValTrpIleValThrSerGluMetSerGlyMetGlnAsp

55 630 640 650 660 670 680
ACTGAGCCAATATTTGAGGAGGAATCCAACCAATTTATTGTCAGAATTGCCAAAGC
ThrGluProIlePheGluGluGluSerLysProIleTyrCysGlnAsnCysGlnSer

60 690 700 710 720 730 740
ATCTCTTTTGTGCATTACACAGAGGTCACTTTGGTTCGTATGCTCCAAATACTGG
IleSerPheCysAlaPheThrGlnArgSerLeuLeuValValCysSerLysTyrTrp

750 760 770 780 790
AGGGTGTTTGATGCTGGCGACTACTCTCTGTTGTGCTCAGGTCTAGTGAAAATGGA
ArgValPheAspAlaGlyAspTyrSerLeuLeuCysSerGlyProSerGluAsnGly

800 810 820 830 840 850
CAGACATGGACTGGAGGGGACTTTGTGTCTGCAGACAAAGTCATCATCTGGACAGAA
GlnThrTrpThrGlyGlyAspPheValSerAlaAspLysValIleIleTrpThrGlu

860 870 880 890 900 910
AATGGGCAGAGTTACATCTACAACTCCCTGCCAGTTGCCCTCCAGCTAGTGATTCA
AsnGlyGlnSerTyrIleTyrLysLeuProAlaSerCysLeuProAlaSerAspSer

920 930 940 950 960
 TTCCGCAGCGACGTGGGGAAGCAGTGGAAAATTTGATCCCTCCTGTGCAGCATAGC
 PheArgSerAspValGlyLysAlaValGluAsnLeuIleProProValGlnHisSer
 5
 970 980 990 1000 1010 1020
 CTCTTGGATCAGAAAGATAAAGAGTTGGTAATTTGTCCTCCTGTTACTCGGTTTTTC
 LeuLeuAspGlnLysAspLysGluLeuValIleCysProProValThrArgPhePhe
 10
 1030 1040 1050 1060 1070 1080
 TACGGATGCAAGGAATATTTGCATAAGCTACTAATTCAGGGCGATTCTTCTGGAAGG
 TyrGlyCysLysGluTyrLeuHisLysLeuLeuIleGlnGlyAspSerSerGlyArg
 15
 1090 1100 1110 1120 1130 1140
 TTAAATATCTGGACATAGCAGACATAGCAGAGAAACAGGAAGCCGATGAAGGGCTA
 LeuAsnIleTrpAsnIleAlaAspIleAlaGluLysGlnGluAlaAspGluGlyLeu
 20
 1150 1160 1170 1180 1190
 AAGATGACAACCTTGTATTAGCTTGCAAGAGGCATTTGACAAGCTGAAGCCTTGCCCT
 LysMetThrThrCysIleSerLeuGlnGluAlaPheAspLysLeuLysProCysPro
 25
 1200 1210 1220 1230 1240 1250
 GCTGGAATTATCGATCAGCTAAGTGTGATTCCCAACAGCAATGAACCTCTTAAAGTA
 AlaGlyIleIleAspGlnLeuSerValIleProAsnSerAsnGluProLeuLysVal
 30
 1260 1270 1280 1290 1300 1310
 ACTGCGAGTGTCTACATACCAGCACACGGGCGACTTGTGTTGGCCGGGAAGATGGA
 ThrAlaSerValTyrIleProAlaHisGlyArgLeuValCysGlyArgGluAspGly
 35
 1320 1330 1340 1350 1360
 AGCATCATTATTGTGCTGCCACCCAGACGGCCATAGTTCAGCTATTGCAAGGAGAA
 SerIleIleIleValProAlaThrGlnThrAlaIleValGlnLeuLeuGlnGlyGlu
 40
 1370 1380 1390 1400 1410 1420
 CACATGCTCAGAAGAGGTGGCCCCCTCACAGAACCTCCCGTGGCCATCGGAACAAA
 HisMetLeuArgArgGlyTrpProProHisArgThrLeuArgGlyHisArgAsnLys
 45
 1430 1440 1450 1460 1470 1480
GTCACGTGCCCTGCTGTATCCCCATCAGGTCTCAGCTCGGTATGACCAAGATACCTG
ValThrCysLeuLeuTyrProHisGlnValSerAlaArgTyrAspGlnArgTyrLeu
 50
 1490 1500 1510 1520 1530
ATATCTGGAGGTGTGGATTTTCCGTCATAATTGGGACATATTTCTGGAGAAATG
IleSerGlyGlyValAspPheSerValIleIleTrpAspIlePheSerGlyGluMet
 55
 1540 1550 1560 1570 1580 1590
 AAACATATCTTCTGTGTTTCATGGTGGTGAGATCACACAACCTCTGGTCCCCCGGAA
 LysHisIlePheCysValHisGlyGlyGluIleThrGlnLeuLeuValProProGlu
 60
 1600 1610 1620 1630 1640 1650
 AACTGTAGTGCAAGAGTTCAACACTGCATCTGTCCGTAGCCAGTGACCACTCTGTA
 AsnCysSerAlaArgValGlnHisCysIleCysSerValAlaSerAspHisSerVal
 65
 1660 1670 1680 1690 1700 1710
 GGCTCTCTAAGTCTGCGAGAGAAAAATGCATCATGTTGGCGTCTCGCCACCTCTTT
 GlyLeuLeuSerLeuArgGluLysLysCysIleMetLeuAlaSerArgHisLeuPhe
 70
 1720 1730 1740 1750 1760
CCTATTCAGGTGATCAAGTGGAGGCCTCCGACGACTACCTGGTGGTGGGATGCACA
ProIleGlnValIleLysTrpArgProSerAspAspTyrLeuValValGlyCysThr
 75
 1770 1780 1790 1800 1810 1820
GACGGCTCTGTGTATGTCTGGCAGATGGACACTGGTGCCTGGATCGTTGTGCAATG

AspGlySerValTyrValTrpGlnMetAspThrGlyAlaLeuAspArgCysAlaMet
 1830 1840 1850 1860 1870 1880
 5 GGAATCACAGCAGTGGAGATACTGAACGCTTGTGACGAAGCCGTTCTCGCCGCTGTA
 GlyIleThrAlaValGluIleLeuAsnAlaCysAspGluAlaValProAlaAlaVal
 1890 1900 1910 1920 1930
 10 GACTCTCTTAGTCATCCAGCAGTCAACCTGAACAAGCCATGACAAGACGGAGTCTC
 AspSerLeuSerHisProAlaValAsnLeuLysGlnAlaMetThrArgArgSerLeu
 1940 1950 1960 1970 1980 1990
 GCTGCCCTTAAAAATATGGCCCACCATAAGCTGCAAACCCCTTGCAACGAACCTTTTG
 AlaAlaLeuLysAsnMetAlaHisHisLysLeuGlnThrLeuAlaThrAsnLeuLeu
 2000 2010 2020 2030 2040 2050
 15 GCTTCTGAGGCCCTCTGACAAGGGTAATTTACCTAAATATTTCCCATAACTCCCTGATG
 AlaSerGluAlaSerAspLysGlyAsnLeuProLysTyrSerHisAsnSerLeuMet
 2060 2070 2080 2090 2100
 20 GTTCAAGCAATAAAGACAAACCTAACAGACCCGGATATCCATGTGCTTTTCTTTGAT
 ValGlnAlaIleLysThrAsnLeuThrAspProAspIleHisValLeuPhePheAsp
 2110 2120 2130 2140 2150 2160
 25 GTGGAAGCTTTGATTATTCAACTCCTGACTGAAGAAGCCTCTAGGCCGAATACTGCA
 ValGluAlaLeuIleIleGlnLeuLeuThrGluGluAlaSerArgProAsnThrAla
 2170 2180 2190 2200 2210 2220
 30 CTTATTTCCCCAGAGAACTGCGAGAAAGCATCTGGCAGTTTCAGACAAAGGGGCTCT
 LeuIleSerProGluAsnLeuGlnLysAlaSerGlySerSerAspLysGlyGlySer
 2230 2240 2250 2260 2270 2280
 35 TTCCTAACTGGGAAGCGAGCAGCGGTTCTTTCCAGCAAGTGAAAGAACTATCAAA
 PheLeuThrGlyLysArgAlaAlaValLeuPheGlnGlnValLysGluThrIleLys
 2290 2300 2310 2320 2330
 GAGAACATAAAGGAACACCTTCTGGATGAGGAGGAGGACGAGGAGGCGGAGGAGG
 GluAsnIleLysGluHisLeuLeuAspGluGluGluAspGluGluGluAlaArgArg
 2340 2350 2360 2370 2380 2390
 40 CAGAGCAGGGAGGATAGTGACCCCTGAGTACCGGGCCAGCAAGTCCAAGCCACTGACC
 GlnSerArgGluAspSerAspProGluTyrArgAlaSerLysSerLysProLeuThr
 2400 2410 2420 2430 2440 2450
 45 CTACTAGAATACACCTTACTATGGATACCGCAAAATTATTTCATGTCTGTCTCCAC
 LeuLeuGluTyrAsnLeuThrMetAspThrAlaLysLeuPheMetSerCysLeuHis
 2460 2470 2480 2490 2500
 50 GCCTGGGGCTTGAATGAAGTTCTGGATGAAGTTGTCTCGATCGCCTCGGAATGCTG
 AlaTrpGlyLeuAsnGluValLeuAspGluValCysLeuAspArgLeuGlyMetLeu
 2510 2520 2530 2540 2550 2560
 AAACCGCACTGCACGGTGTCTTTGGTCTCCTATCGAGAGGAGGTATATGTCTGCTG
 LysProHisCysThrValSerPheGlyLeuLeuSerArgGlyGlyHisMetSerLeu
 2570 2580 2590 2600 2610 2620
 55 ATGCTTCCCGGTTATAATCAGGCTGCTGGAAACTGCTGCATGCGAAAGCAGAAGTA
 MetLeuProGlyTyrAsnGlnAlaAlaGlyLysLeuLeuHisAlaLysAlaGluVal
 2630 2640 2650 2660 2670
 60 GGAAGGAAGCTGCCAGCAGCGGAGGGCGTAGGCAAGGGAACCTACACAGTGTCTCGA
 GlyArgLysLeuProAlaAlaGluGlyValGlyLysGlyThrTyrThrValSerArg
 2680 2690 2700 2710 2720 2730

GCGGTCACCACTCAGCATCTGTTGTCCATCATATCCCTGGCGAATACTTTAATGAGT
 AlaValThrThrGlnHisLeuLeuSerIleIleSerLeuAlaAsnThrLeuMetSer
 2740 2750 2760 2770 2780 2790
 ATGACCAATGCAACTTTCATTGGCGATCACATGAAGAAGGGCCCCACAGGCCGCCT
 5 MetThrAsnAlaThrPheIleGlyAspHisMetLysLysGlyProThrArgProPro
 2800 2810 2820 2830 2840 2850
 AGACCTGGCACCCAGACCTCTCTAAGGCGAGGGATTCCCCTCCAGCTCCAGTAAC
 10 ArgProGlyThrProAspLeuSerLysAlaArgAspSerProProAlaSerSerAsn
 2860 2870 2880 2890 2900
 ATTGTGCAAGGACAGATTAAACAAGCCGCTGCGCCTGTCGTTTCTGCTCGGTCTGAC
 15 IleValGlnGlyGlnIleLysGlnAlaAlaAlaProValValSerAlaArgSerAsp
 2910 2920 2930 2940 2950 2960
 GCTGATCACTCTGGCTCTGACTCTGCCTCTCCTGCTTTACCTACCTGTTTCTTAGTA
 AlaAspHisSerGlySerAspSerAlaSerProAlaLeuProThrCysPheLeuVal
 2970 2980 2990 3000 3010 3020
 AATGAAGGCTGGAGCCAGTTAGCCGCCATGCACTGTGTATGTTGCCTGACCTGCTG
 20 AsnGluGlyTrpSerGlnLeuAlaAlaMetHisCysValMetLeuProAspLeuLeu
 3030 3040 3050 3060 3070
 GGGCTGGAGAGATTACAGCCTCCTCTCCTGGAGATGCTAGCTCGAAGATGGCAGGAC
 25 GlyLeuGluArgPheArgProProLeuLeuGluMetLeuAlaArgArgTrpGlnAsp
 3080 3090 3100 3110 3120 3130
 CGATGCTTGGAGGTGAGAGAGGCTGCACAGGCCCTGCTTCTAGCTGAGCTGAGAAGG
 30 ArgCysLeuGluValArgGluAlaAlaGlnAlaLeuLeuLeuAlaGluLeuArgArg
 3140 3150 3160 3170 3180 3190
 ATTGAGCAGGCAGGACGGAAGGAGACGATCGACACCTGGGCTCCTTACTTACCTCAG
 35 IleGluGlnAlaGlyArgLysGluThrIleAspThrTrpAlaProTyrLeuProGln
 3200 3210 3220 3230 3240
 TATATGGACCATGTCATATCACCTGGCGTCACGGCGGAAGCCATGCAGACTATGGCA
 TyrMetAspHisValIleSerProGlyValThrAlaGluAlaMetGlnThrMetAla
 3250 3260 3270 3280 3290 3300
 GCTGCTCCAGATGCCTCGGGCCCAGAAGCCAAAGTCCAGGAAGAAGCATGACCTG
 40 AlaAlaProAspAlaSerGlyProGluAlaLysValGlnGluGluGluHisAspLeu
 3310 3320 3330 3340 3350 3360
 GTGGATGATGACATCACTGCAGGTTGCTTGTCAAGTGTCCCACAGATGAAAAAATC
 45 ValAspAspAspIleThrAlaGlyCysLeuSerSerValProGlnMetLysLysIle
 3370 3380 3390 3400 3410 3420
 TCCACGTCTTACGAAGAAAGAAGGAAGCAGGCCACGGCTATTGTTCTCTGGGAGTG
 50 SerThrSerTyrGluGluArgArgLysGlnAlaThrAlaIleValLeuLeuGlyVal
 3430 3440 3450 3460 3470
 ATAGGGGCAGAGTTTGGAGCTGAAATTGAACCGCCGAAGCTGCTGACCAGGCCCTCGA
 55 IleGlyAlaGluPheGlyAlaGluIleGluProProLysLeuLeuThrArgProArg
 3480 3490 3500 3510 3520 3530
 AGCTCCAGTCAAATCCCTGAAGGCTTTGGCTTGACCAGCGGAGGCTCCAATACTCTC
 SerSerSerGlnIleProGluGlyPheGlyLeuThrSerGlyGlySerAsnTyrSer
 3540 3550 3560 3570 3580 3590
 CTGGCCAGACACAGTCAAGGCACTGACATATCTTCTGCTACAGCCACCAAGTCCC
 60 LeuAlaArgHisThrCysLysAlaLeuThrTyrLeuLeuLeuGlnProProSerPro

3600 3610 3620 3630 3640
AAGCTCCCTCCTCATAGCACCATCCGGAGAACTGCCACTGACCTGATTGGGCGAGGG
LysLeuProProHisSerThrIleArgArgThrAlaThrAspLeuIleGlyArgGly

5 3650 3660 3670 3680 3690 3700
TTCACCTGTATGGGAGCCCTACATGGATGTGTCCGCTGTCTCATGGGGCTGCTGGAG
PheThrValTrpGluProTyrMetAspValSerAlaValLeuMetGlyLeuLeuGlu

10 3710 3720 3730 3740 3750 3760
CTCTGTGCAGACGCTGAGAAACAACCTGCCAACATCACAATGGGGCTGCCCTCTGAGC
LeuCysAlaAspAlaGluLysGlnLeuAlaAsnIleThrMetGlyLeuProLeuSer

15 3770 3780 3790 3800 3810
CCTGCAGCTGACTCTGCCCCTCCGCAAGGCACGCCCTGTCTCTCATCGCCACAGCC
ProAlaAlaAspSerAlaArgSerAlaArgHisAlaLeuSerLeuIleAlaThrAla

20 3820 3830 3840 3850 3860 3870
AGACCACCCGCTTCATCACCACCATAGCTAAGGAGGTCCACAGACACACGGCCCTT
ArgProProAlaPheIleThrThrIleAlaLysGluValHisArgHisThrAlaLeu

25 3880 3890 3900 3910 3920 3930
GCAGCGAACACCCAGTCCCAGCAGATATACACACCACACCTGGCGAGGGCTAAA
AlaAlaAsnThrGlnSerGlnGlnSerIleHisThrThrThrLeuAlaArgAlaLys

30 3940 3950 3960 3970 3980 3990
GGCGAAATCCTGAGAGTCATTGAAATTCATTGAAAAGATGCCACGGATGTGGTG
GlyGluIleLeuArgValIleGluIleLeuIleGluLysMetProThrAspValVal

35 4000 4010 4020 4030 4040
GATCTTCTTGTGGAGGTGATGGATATCATCATGTACTGCCTGGAAGGATCTTAGTG
AspLeuLeuValGluValMetAspIleIleMetTyrCysLeuGluGlySerLeuVal

40 4050 4060 4070 4080 4090 4100
AAAAAGAAGGGTCTTCAGGAGTGTTCAGCTATCTGCAGGTTCTACATGGTCAGC
LysLysLysGlyLeuGlnGluCysPheProAlaIleCysArgPheTyrMetValSer

45 4110 4120 4130 4140 4150 4160
TATTATGAGCGCAGTCACAGAATCGCAGTTGGAGCAGCCATGGCTCAGTAGCCCTG
TyrTyrGluArgSerHisArgIleAlaValGlyAlaArgHisGlySerValAlaLeu

50 4170 4180 4190 4200 4210
TATGACATCCGGACTGGAAAATGTCAGACAATCCATGGGCACAAGGACCAATCAGC
TyrAspIleArgThrGlyLysCysGlnThrIleHisGlyHisLysGlyProIleThr

55 4220 4230 4240 4250 4260 4270
GCGGTGTCTTTGCTCCTGATGGCCGTTACCTTGCCACCTACTCGAACACCGACAGC
AlaValSerPheAlaProAspGlyArgTyrLeuAlaThrTyrSerAsnThrAspSer

60 4280 4290 4300 4310 4320 4330
CACATTTCCCTTCTGGCAGATGAACACCTCACTCCTGGGAAGCATTGGAATGCTGAAC
HisIleSerPheTrpGlnMetAsnThrSerLeuLeuGlySerIleGlyMetLeuAsn

4340 4350 4360 4370 4380
TCAGCTCCTCAGCTGCGCTGCATCAAGACCTACCAGGTCCCTCCAGTGCAGCCAGCA
SerAlaProGlnLeuArgCysIleLysThrTyrGlnValProProValGlnProAla

4390 4400 4410 4420 4430 4440
TCCCCTGGCTCCACACAACGCCCTTAAGTTGGCCCGGCTCATCTGGACTTCCAACCGG
SerProGlySerHisAsnAlaLeuLysLeuAlaArgLeuIleTrpThrSerAsnArg

4450 4460 4470 4480 4490
AATGTTATCCTCATGGCCCATGATGGGAAGGAACACCGCTTCATGGTCTGA
AsnValIleLeuMetAlaHisAspGlyLysGluHisArgPheMetValSTP

Table 4 shows a comparison of the amino acid sequence of the rat brain (SEQ ID NO: 2), murine brain (SEQ ID NO: 6), and human brain (SEQ ID NO: 4) TRAG

5 proteins. The sequence specific only to brain TRAG is at positions 951 to 981 in the rat (top), 951 to 980 in the mouse (middle), and 951 to 982 in the human (bottom).

	1	MAGNSLVLPVLWGRKAPTHCISILLTDDGGTIVTGCHDGGICLWDVSVLEVNPRALL	60
	1	MAGNSLVLPVLWGRKAPTHCISILLTDDGGTIVTGCHDGGICLWDLSEELVNPRALL	60
10	1	MAGNSLVLPVLWGRKAPTHCISAVLLTDDGATIVTGCHDGGICLWDLSVELQVNPRALL	60
	61	FGHTASITCLSKACASGDKRYTVSASANGEMCLWDVNDGRCIEFTKLACTHTGTGIFYQFS	120
	61	FGHTAAITCLSKACASGDKRYTVSASANGEMCLWDVNDGRCIEFTKLACTHTGTGIFYQFS	120
	61	FGHTASITCLSKACASSDKQYIVSASESGEMCLWDVSDGRCIEFTKLACTHTGTGIFYQFS	120
15	121	VGNQOEGRLLCHGHYPEILVVDATSLVLYSLVSKISPDWISSMSIIHSQRTQEDTVVAL	180
	121	VGNQREGRLCHGHYPEILVVDATSLVLYSLVSKISPDWISSMSIIRSHRTQEDTVVAL	180
	121	VGNQREGRLCHGHYPEILVVDATSLVLYSLVSKISPDWISSMSIIRSHRTQEDTVVAL	180
20	181	SVTGILKVWIVTSEMSGMDTEPIFEEESKPIYCQNCQSISFCAFTQRSLLVVCISKYWRV	240
	181	SVTGILKVWIVTSEISGLQDTEPIFEEESKPIYCQNCQSLSFCAFTQRSLLVVCISKYWRV	240
	181	SVTGILKVWIVTSEISDMQDTEPIFEEESKPIYCQNCQSISFCAFTQRSLLVVCISKYWRV	240
	241	FDAGDYSLLCSGSPSENGQTWTGGDFVSADKVIWTENGQSYIYKLPASCLPASDSFRSDV	300
	241	FDAGDYSLLCSGSPSEDGQTWTGGDFVSADKVIWTENGQSYIYKLPASCLPASDSFRSDV	300
25	241	FDAGDYSLLCSGSPSENGQTWTGGDFVSSDKVIWTENGQSYIYKLPASCLPASDSFRSDV	300
	301	GKAIVENLIPPVQHSLLDQKDELVICPPVTRFFYGCKEYLHKLLIQGDSSGRLLNIWNIAD	360
	301	GKAIVENLIPPVQHSLLDQKRELVICPPVTRFFYGCKEYLHKLLIQGDSSGRLLSIWNIAD	360
30	301	GKAIVENLIPPVQHILLDRKDKELLICPPVTRFFYGCREYFHKLLIQGDSSGRLLNIWNIAD	360
	361	IAEKQEADEGLKMTTCISLQEAFDKLPKCPAGIIDQLSVIPNSNEPLKVTASVYIPAHGR	420
	361	IADKQEADEGLKMTTCISLQDAFDKLPKCPAGIIDQLSVIPNSNEPLKVTASVYIPAHGR	420
	361	TADKQGESEGLAMTTTISLQEAFDKLPKCPAGIIDQLSVIPNSNEPLKVTASVYIPAHGR	420
35	421	LVCGREDSIIIVPATQTAIVQLLQGEHMLRRGWPPHRTLGRHRNKVTCLLYPHQVSARY	480
	421	LVCGREDSIIIVPATQTAIVQLLQGEHMLRRGWPPHRTLGRHRNKVTCLLYPHQVSARY	480
	421	LVCGREDSIIVPATQTAIVQLLQGEHMLRRGWPPHRTLGRHRNKVTCLLYPHQVSARY	480
40	481	DQRYLISGGVDFSVIWDIFSGEMKHIFCVHGGEITQLLVPPENCARSVQHCICSVASDH	540
	481	DQRYLISGGVDFSVIWDIFSGEMKHIFCVHGGEITQLLVPPENCARSVQHCVCVSDH	540
	481	DQRYLISGGVDFSVIWDIFSGEMKHIFCVHGGEITQLLVPPENCARSVQHCICSVASDH	540
45	541	SVGLLSLREKKCIMLASRHLFPQVIKWRPSDDYLVVGCTDGSVYVWQMDTGALDRCAMG	600
	541	SVGLLSLREKKCIMLASRHLFPQVIKWRPSDDYLVVGCTDGSVCVWQMDTGALDRCAMG	600
	541	SVGLLSLREKKCIMLASRHLFPQVIKWRPSDDYLVVGCSGDSVYVWQMDTGALDRCVMG	600
50	601	ITAVEILNACDEAVPAVDSLSHPAVNLQAMTRRSALAKNMAHHKLQTLATNLLASEA	660
	601	ITAVEILNACDEAVPAVDSLSHPAVNLQAMTRRSALAKNMAHHKLQTLATNLLASEA	660
	601	ITAVEILNACDEAVPAVDSLSHPAVNLQAMTRRSALAKNMAHHKLQTLATNLLASEA	660
	661	SDKGNLPHYSHNSLMVQAIKTNLTDPIHVLFFDVEALIIQLLTEEASRPNTALISPENL	720
	661	SDKGNLPHYSHNSLMVQAIKTNLTDPIHVLFFDVEALIIQLLTEEASRPNTALISPENL	720
	661	SDKGNLPHYSHNSLMVQAIKTNLTDPIHVLFFDVEALIIQLLTEEASRPNTALISPENL	720
55	721	QKASGSSDKGGSFLTGKRAAVLFQOVKETIKENIKEHLLDEEEDDEEARRQSRSDPEY	780
	721	QKASGSSDKGGSFLTGKRAAVLFQOVKETIKENIKEHLLDEEEDDEEVMRQRRESDPEY	780
	721	QKASGSSDKGGSFLTGKRAAVLFQOVKETIKENIKEHLLDEEEDDEEIMRQRRESDPEY	780
	781	RASKSKPLTILEYNLTMDTAKLFMSCLHAWGLNEVLDEVCLDRLGMLKPHCTVSFGLLSR	840

	781	RASKSKPLTLLEYNLMTDAKLFMSCLHAWGLNEVLDEVCLDRGLMKPHCTVSFGLLSR	840
	781	RSKSKPLTLLEYNLMTDAKLFMSCLHAWGLNEVLDEVCLDRGLMKPHCTVSFGLLSR	840
5	841	GGHMSMLPGYNQAAGKLLHAKAEVGRKLPAAEGVGKGYTVSRAVTTQHLLSIISLANT	900
	841	GGHMSMLPGYNQAAGKLLQAKAEAGRKGPATESVGKGYTVSRAVTTQHLLSIISLANT	900
	841	GGHMSMLPGYNQPACKLSHGKTEVGRKLPASEGVGKGYTVSRAVTTQHLLSIISLANT	900
	901	LMSMTNATFIGDHMKKGPTRP RPPTDLSKARDSPPASSNIVQGQIKQAAAPVVSARSD	960
	901	LMSMTNATFIGDHMKKGPTRP RPPTDLSKARDSPPASSNIVQGQIKQAAAP-VSARSA	959
10	901	LMSMTNATFIGDHMKKGPTRP RPSTPDL SKARGSPPTSSNIVQGQIKQVAAAPVVSARSD	960
	961	ADHSGSDS-ASPALPTCLFVNEGWSQLAAMHCVMPLDLLGLERFRPPLLEMLARRWQDRC	1019
	960	ADHSGSAS-ASPALRTCLFVNEGWSQLAAMHCVMPLDLLGLGKFRPPLLEMLARRWQDRC	1018
	961	ADHSGSDPPSAPALHTCLFVNEGWSQLAAMHCVMPLDLLGLDKFRPPLLEMLARRWQDRC	1020
15	1020	LEVREAAQALLLAE LRRIEQAGRKETIDTWAPYLPQYMDHVISP GVTAEAMQTMAAAPDA	1079
	1019	LEVREAAQALLLAE LRRIEQAGRKETIDTWAPYLPQYMDHVISP GVTAEAMQTMAAAPDA	1078
	1021	LEVREAAQALLLAE LRRIEQAGRKEAIDAWAPYLPQYIDHVISP GVTSEAAQTITAPDA	1080
20	1080	SGPEAKVQEEHDLVDDITAGCLSSVPQMKKISTSYEERRKQATAIVLLGVIGAEFGAE	1139
	1079	SGPEAKVQEEHDLVDDITGCLSSVPQMKKMSTSYEERRKQATAIVLLGVIGAEFGAE	1138
	1081	SGPEAKVQEEHDLVDDITGCLSSVPQMKKISTSYEERRKQATAIVLLGVIGAEFGAE	1140
25	1140	IEPPKLLTRPRSSSQIPEGFGLTSGGSNYSLARHTCKALTYLLLQPPSPKLP PPHSTIRRT	1199
	1139	IEPPKLLTRPRSSSQIPEGFGLTSGGSNYSLARHTCKALTFLLLQPPSPKLP PPHSTIRRT	1198
	1141	IEPPKLLTRPRSSSQIPEGFGLTSGGSNYSLARHTCKALTFLLLQPPSPKLP PPHSTIRRT	1200
	1200	ATDLIGRGFTVWEPYMDVSAVLMGLLELCADA EKQLANITMGLPLSPAADSARSARHALS	1259
	1199	AIDLIGRGFTVWEPYMDVSAVLMGLLELCADA EKQLANITMGLPLSPAADSARSARHALS	1258
30	1201	AIDLIGRGFTVWEPYMDVSAVLMGLLELCADA EKQLANITMGLPLSPAADSARSARHALS	1260
	1260	LIATARPPAFITTTIAKEVHRHTALAANTOSQOSIHTTTLARAKGEILRVIEILIEKMPTD	1319
	1259	LIATARPPAFITTTIAKEVHRHTALAANTOSQOSIHTTTLARAKGEILRVIEILIEKMPTD	1318
	1261	LIATARPPAFITTTIAKEVHRHTALAANTOSQONMHTTTLARAKGEILRVIEILIEKMPTD	1320
35	1320	VVDLLVEVMDIIMYCLEGSLVKKKGLQECFPAICRFYMVSYYERSHRIAVGARHG SVALY	1379
	1319	VVDLLVEVMDIIMYCLEGSLVKKKGLQECFPAICRFYMVSYYERSHRIAVGARHG SVALY	1378
	1321	VVDLLVEVMDIIMYCLEGSLVKKKGLQECFPAICRFYMVSYYERNHRIAVGARHG SVALY	1380
40	1380	DIRTGKCQTIHGHKGPI TAVSFAPDGRYLATYSNTDSHISFWQMNTSLLGSIGMLNSAPQ	1439
	1379	DIRTGKCQTIHGHKGPI TAVSFAPDGRYLATYSNTDSHISFWQMNTSLLGSIGMLNSAPQ	1438
	1381	DIRTGKCQTIHGHKGPI TAVAFAPDGRYLATYSNTDSHISFWQMNTSLLGSIGMLNSAPQ	1440
	1440	LRCIKTYQVPPVQPASPGSHNALKLARLIWTSNRNVILMAHDGKEHRE FMV	1489
45	1439	LRCIKTYQVPPVQPASPGSHNALKLARLIWTSNRNVILMAHDGKEHRE FMV	1488
	1441	LRCIKTYQVPPVQPASPGSHNALKLARLIWTSNRNVILMAHDGKEHRE FMV	1490

Table 5 shows a comparison of the amino acid sequence of murine (SEQ ID NO: 50 6) and Drosophila TRAG (SEQ ID NO:7) proteins. Drosophila protein sequence obtained by translating noncontiguous regions of Drosophila genomic sequence (GenBank Accession Number AL021086).

	1	MAGNSLVLPVIVLWGRKAPTHCISILLTDDGGTIVTGCHDGQICLWDVS-VELEVNPRAL	59
55	1	MVSTNLVVPVVLWGPTAPTHCISVFLSDDQFTLVTCGYDGGIXLWQVEPTTLKMSPRCL	60
	60	LFGHTASITCLSKACASGDKRYTVSASANGEMCLWDVNDGRCEFTKLACTHTGIQFYQF	119
	61	LVGHSAPVLCLVRASLLPENNFLVSSSENGEMCTWDLTDGKCM EAVKLPQVHTQIQSYHT	120
	120	SVGNQQEGRLLCHGHYPEILVVDATSL EVLVSLVSKISPDWISSMSIIHSQRTQEDTVVA	179

	121	--ANSEDVRLFCIGYYAEIMVMDPFSLEVIYVLSSKVKPDWISAIHVLPRMRKDDVLA	178
	180	LSVTGILKVWIVTSEMSGMDTEPIFEESKPIYCQNCQSISFCAFTQRSLLVVCCKYWR	239
5	179	ITTTGTVKVWTLTGNN--KHAEPIYENESKEIRCLNAITMCCAQNQRTVLLVCTKYWQ	236
	240	VFDAGDYSLLCSGSPSENGQTWTGGDFVSADKVIWTENGQSYIYKLPASCLPASDSFRSD	299
	237	IYDAGDFTVLCVIAPARERWQGGDFITSDRVMLWTDEGKGLYKLPANCIPDNKEFHS-	295
10	300	VGKAVERNLIIPPVQHSLLDQKDKELVICPPVTRFFYGCKEYLHKLLIQGDSSGRLNIWNIA	359
	296	--KSVVRDAPYLYYVLQHAGDK-VLSCFPAMKLLQGAGG-QHNLLR-GDSEGYISVWNV	350
	360	DIAE-----KQEADEGLKMTTCISLQEAQFDKLPKCPAGIIDQLSVIPNSNEPLKVTA	411
	351	EVPLDNISILQAKQMPRPLKPHVCTSLVEAWSIMDPPVVGILDQLSRITES--PVKLT	408
15	412	SVYIPAHGRLVCGREDGSIIVPATQTATVQLLQGEHMLRRGWPPHRTLGRHNRKVTCLL	471
	409	SIYLPQQSRLVIGREDGSIVIVPATQTVMMQLLVGKQNFSDWPSHQILYGRGRVNCCL	468
	472	YPHQVSARYDQRYLISGGVDFSVIWDIFSGEMKHIFCVHGGEITQLLVPPENC SARVQH	531
20	469	CPSMIHSRYEKSHLLSGGIDFAVCLWDLYSGSLLHRFCVHAGEITQLLVPPESCSPRILK	528
	532	CICSVASDHSVGLLSLREKKCIMLASRHLFPQVIKWRPDDYLVVGCTDGSVYVWQMDT	591
	529	CICSVASDHSVTLVSLQERKCVTLASRHLFPVVTIKWAPLDDFLIVGCSGDSVYVWQMET	588
25	592	GALDRCAMGITAVEILNACDEAVP-----AAVDSLSPAVNLKQAMTRRSL	637
	589	GHLDRVLHGMLAEVLSACDEQAEDGGSGGGSGNGASASEMGMANPAVHFFRGLKSRNM	648
	638	AALKNMAHKLQTLATNLLASEASDKGN---LPKYSHNSLMVQAIKTNLTDPDIHVLFDD	694
	649	NAIR----HATQRGITQLQQLQGHNGNFDFLMKHRSNPLVIQGLRTNPKDAESHILFDD	704
30	695	VEALIIQLLTEEASRPNTALISPENLQKASGSSDKGGSFLTGKRAAVLFQOVK-----E	748
	705	IEGLIFELHSEEYAQMTPATLES LGVHLQNPKGKSMMLDASKKIGDFNFKVKNKAVDVE	764
	749	TIKENIKEHLDEEEDDEE---EARRQSRDS-----DP--EYRASKSKPLTILEYNLTM	797
35	765	KILKDKDKHGLVQKFKEKTEIVEKKVQAKVESLQKAVEPHEEQDLKSKIASKMEVTHVM	824
	798	DTAKLFMSCLHAWGLNEVLDEVCLDRLGMLKPHCTVSFGLLSRGGHMSMLP----GYNQ	853
	825	EVAQLLLSLLHSWGLDPLDKMCETRLGLLRPIVPISYGVLSKAGYMSLLLPWQNNYAI	884
40	854	AAGKLLHAKAEVGRKLP-----AAEGVGKGTYYTVSRAVTTQHLLSIISLANTILMSM	904
	885	PPGIQLPSSSK-RPLPEELQRLHETAVFTSRHLWELSTTLTNHILALVAMSNTLLSM	943
	905	TNATFIGDHMKGPTRPPRPGTPDLKARDSPPASSNIVQGQIKQAAAPVVSARSADHS	964
	944	SAASFLLPDEK--HKKLQR-----LAQRDS--TLSNEE-----REELMAHHI	983
45	965	GSDSASPALPTCFLVNEGWSQLAAMHCVMPLD--LLGLE--RFRPPLLEMLARRWQDRCL	1021
	984	SQ-----IKHAWSLATHHCFLLPDKIEALEPKKFKRPQVEMMVKRWQHHCIE	1031
	1022	VREAAQALLLAELRRIEQAGRKETIDTWAPYLPQYMDHVISPGVTAEAMQTMAAAPDASG	1081
50	1032	IREAAQQILLGELTRMGKKGRKQLVESWAQYLPYLT-HT-EPIVGAQQQLALISQPASGG	1089
	1082	PEAKVQEEHDLVDDIT----AGCLS----SVP-----Q-----MKKISTSYE	1117
	1090	--AGSGSGNGGVGVGVSGGGGAGSGSGPGGDAHQDEDEYEEEEIEIRKPSSLSE	1147
	1118	ERRKQATAIVLLGVIGAEFGAEI--EPP-----KLLTR-----PRSSSQIEGEF	1159
55	1148	LKRKQTTAVILLGVIGAEFGQDISQESPNHRGSISMATGANLTSGVAGGERKSSVVEGF	1207
	1160	GLTSGGSNYSLARHTCKALTYLLQPPSPKLPHPSTIRRTATDLIGRGFTVWEPYMDVSA	1219
	1208	GIAN-----NLARLTSMALAHLLYAPPSPKLPQYTPLRRAIDLLGRGFTVWEPYLDVSK	1262
60	1220	VLMGLLELCADAQKLANITMGLPLSPAADSARSARHALSLIATARPPAFITTIKEVHR	1279
	1263	VLLGLLEISCEG-KAVPNLNYKPLTPQADACTARHALRLIATARPAAFITTMAREVAR	1321
	1280	HTALAANTQSQQS-IHTTLARAKGEILRVIEILIEKMPTDVPDLLVEVMDIIMYCLEGS	1338

1322 YNTMQQNAQSINTPLTQSVLHKAKGEILQCVEMLIDKMQSEIAGLLVEVMDIALHCVDGN 1381

1339 LVKKKGLQECFPAICRFYMVSYERSHRIAVGARHGSVALYDIRTGKCQTIHGHKGPIA 1398

1382 ELKNRGLAELCPAICKFNQISHCAQTRRIAVGANSGNLAIYELRQNKQMPIANHPITS 1441

5 1399 VSFAPDGRYLATYSNTDSHISFWQMNTSLLGSIGMLNSAPQLRCIKTYQVPPVQPASPGS 1458

1442 LAFSPDGKYLVSYSACENRLSFWQTSTGMFG----LGQS-QTRCTKGYSTAPIPDVS--R 1494

1459 HNALKLARLIWTSNRNVILMAHDGKEHRFMV 1489

10 1495 LNPMLAKLVWINNRTVTMLADGSETRFNV 1525

The Claimed Invention Is:

1. An isolated polypeptide comprising a TRAG polypeptide fragment, said fragment comprising a fragment of an amino acid sequence as shown in Table 1, 2, or 3.
2. The TRAG polypeptide fragment of claim 1, wherein said TRAG polypeptide fragment is a full-length TRAG polypeptide comprising an amino acid sequence as shown in Table 1, 2, or 3.
3. The TRAG polypeptide fragment of claim 1, further comprising a tyrosine phosphorylation motif.
4. The TRAG polypeptide fragment of claim 1, further comprising a WD-repeat-element motif.
5. The TRAG polypeptide fragment of claim 1 joined to a detectable label.
6. The TRAG polypeptide fragment of claim 5, wherein the detectable label includes a radioactive isotope, an enzyme, a chromophore, or a mixture thereof.
7. An isolated nucleic acid sequence encoding a TRAG polypeptide fragment, said
TRAG
fragment comprising a fragment of an amino acid sequence as shown in Table 1, 2, or 3.
8. The nucleic acid sequence of claim 7, comprising a nucleotide sequence coding for an amino acid sequence as shown in Table 1, 2, or 3.
9. The nucleic acid sequence of claim 7, wherein the nucleic acid sequence is codon optimized for a specific host cell.
10. The nucleic acid sequence of claim 7 joined to a detectable label.
11. The nucleic acid sequence of claim 7, wherein said nucleic acid sequence is DNA.
12. The nucleic acid sequence of claim 11, wherein the DNA is cDNA.

13. The nucleic acid sequence of claim 7, wherein the nucleic acid sequence is RNA.
14. The nucleic acid sequence of claim 13, wherein the RNA is mRNA.
15. A vector comprising a polynucleotide encoding the TRAG polypeptide fragment of claim 1.
16. The vector of claim 15, wherein the nucleic acid is operably linked to at least one control sequence capable of being recognized by a host cell transformed with the vector.
17. A host cell comprising the vector of claim 16.
18. A process for producing TRAG polypeptide fragments comprising culturing the host cell of claim 17 under conditions such that the TRAG polypeptide fragment is produced.
19. A TRAG polypeptide fragment produced by the method of claim 18.
20. A TRAG antisense oligonucleotide comprising a nucleotide sequence that is complementary to an mRNA encoding a polypeptide comprising a TRAG polypeptide fragment of claim 1.
21. A chimeric molecule comprising a TRAG polypeptide fragment of claim 1 fused to a heterologous amino acid sequence.
22. An isolated TRAG specific polypeptide comprising an F_{ab} fragment from an antibody capable of specifically binding to a TRAG polypeptide fragment of claim 1.
23. The isolated TRAG specific polypeptide of claim 22, wherein said polypeptide comprises an isolated antibody.
24. The TRAG specific polypeptide of claim 23, wherein said antibody is a polyclonal, monoclonal, or chimeric antibody.

25. A method of assaying a sample for a polynucleotide encoding a TRAG polypeptide fragment comprising detecting the presence or absence of said polynucleotide in said sample utilizing a nucleic acid probe capable of hybridizing with the nucleic acid sequence of claim 7.
26. A method of assaying a sample for a TRAG polypeptide fragment of claim 1 comprising detecting the presence or absence of said TRAG polypeptide fragment in said sample utilizing an isolated TRAG specific polypeptide, said TRAG specific polypeptide comprising a F_{ab} fragment from an antibody capable of specifically binding to the TRAG polypeptide fragment.
27. A method of reducing expression of a TRAG polypeptide fragment of claim 1 in a cell comprising exposing the cell to an oligonucleotide of at least about 15 nucleotides which are complementary to a TRAG mRNA.
28. A method for producing cell lines having an altered phenotype comprising:
- (i) transfecting in vitro mammalian cells with a DNA vector encoding a TRAG polypeptide fragment of claim 1;
 - (ii) expressing the TRAG polypeptide fragment in said cells; and
 - (iii) selecting for cells having an altered phenotype.

FIG. 1B

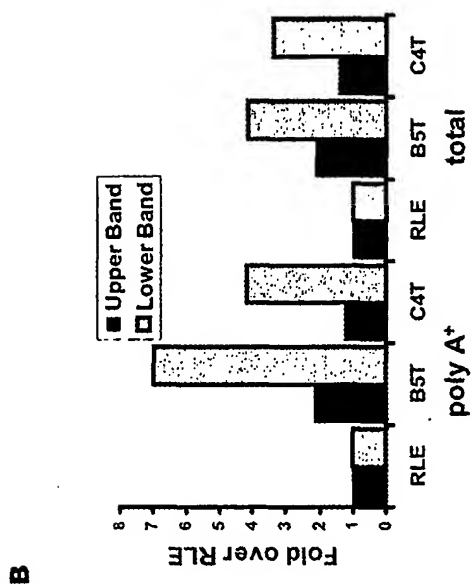


FIG. 1A

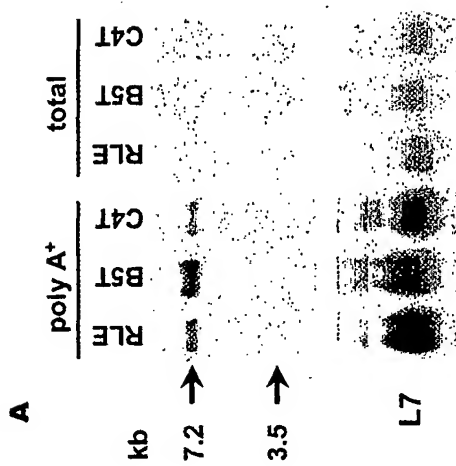
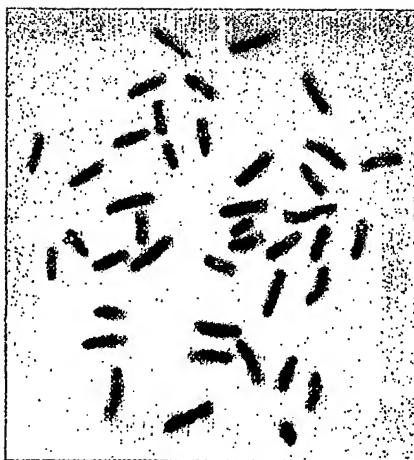


FIG. 2A



Mouse Ch. 18 paint



TRAG probe

FIG. 2B



Human Ch. 18 paint



TRAG probe

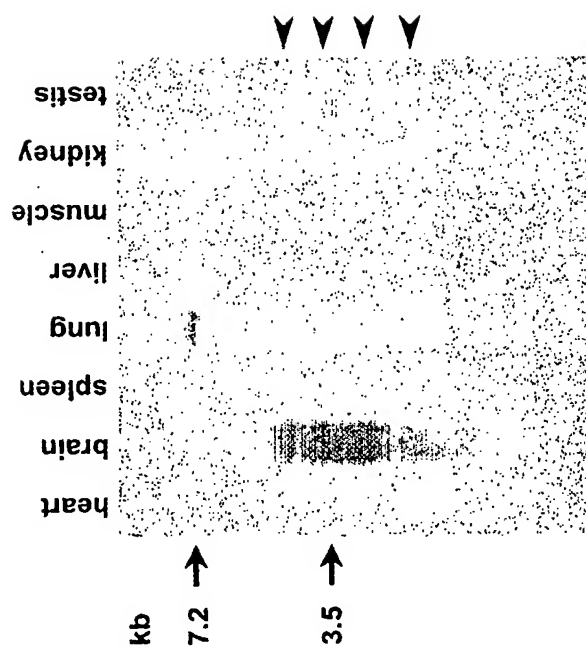


FIG. 3A

FIG. 3C

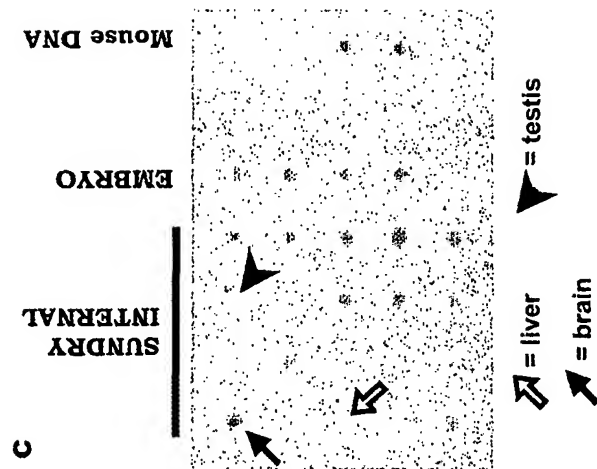
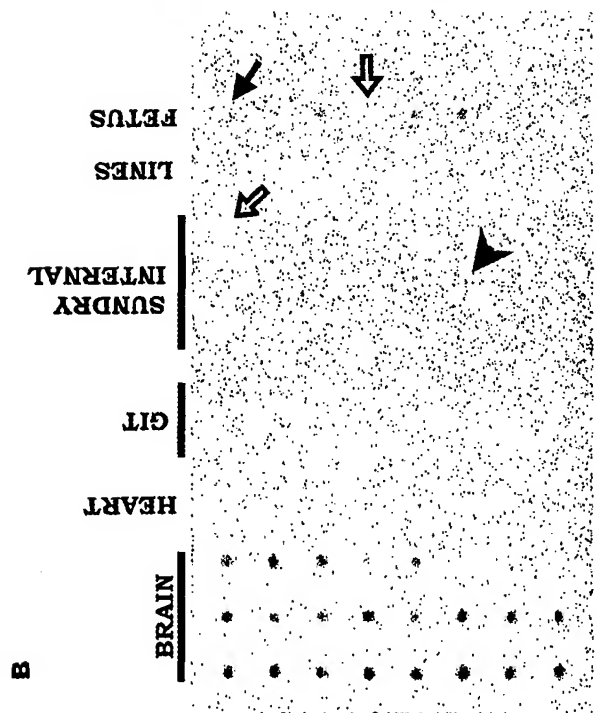


FIG. 3B



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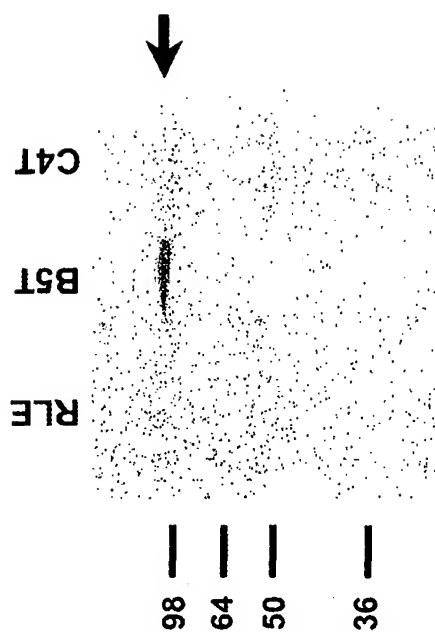


FIG. 4

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FIG. 5B

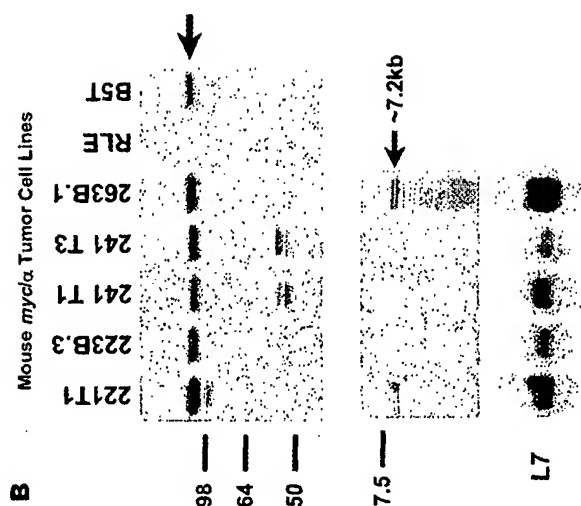
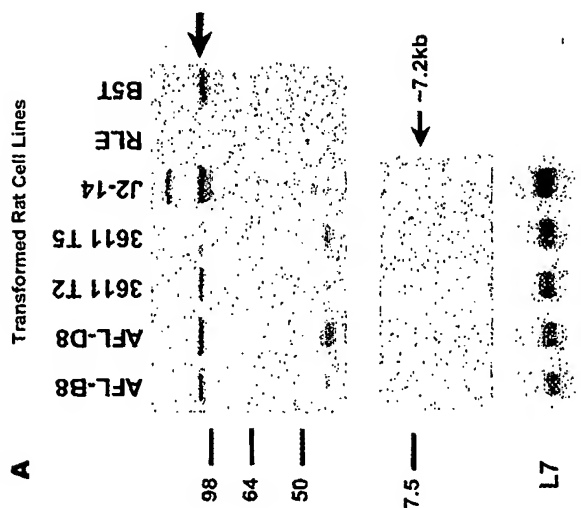
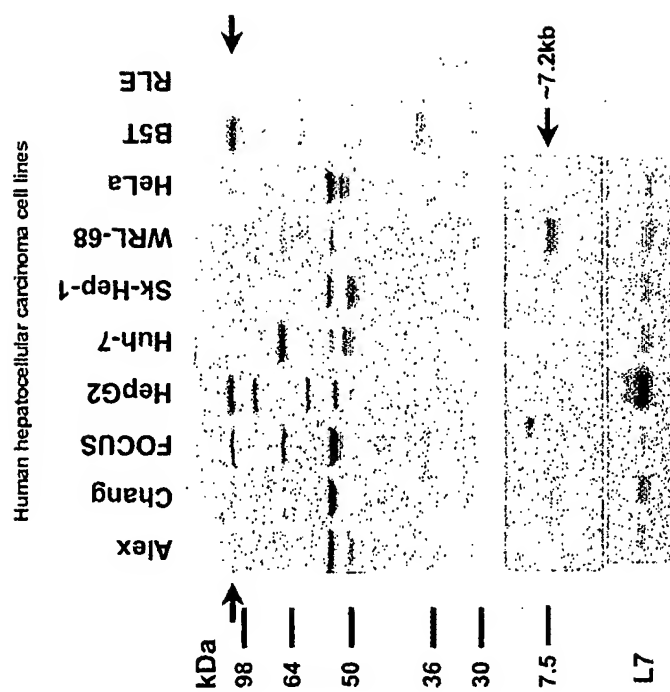


FIG. 5A



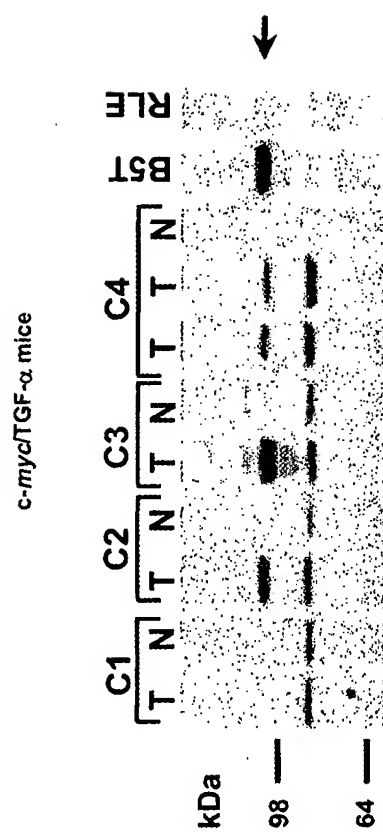
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FIG. 5C



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FIG. 5D



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FIG. 6A

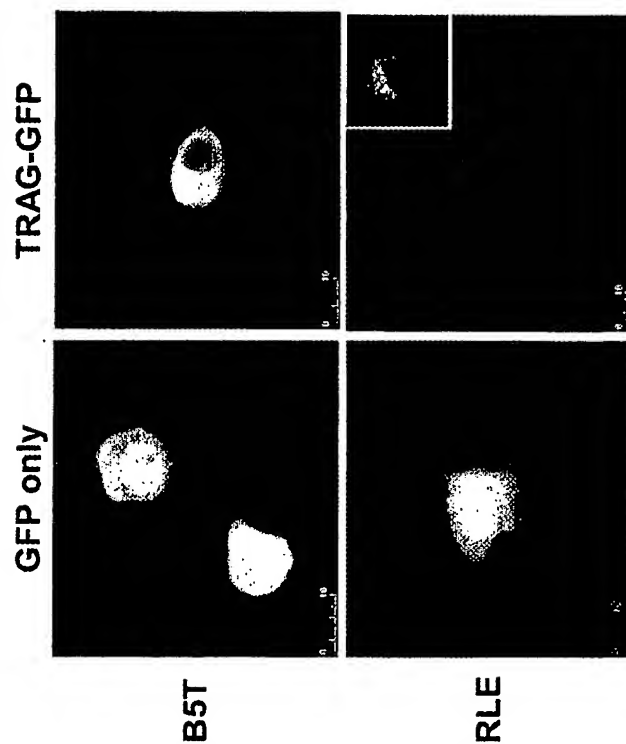
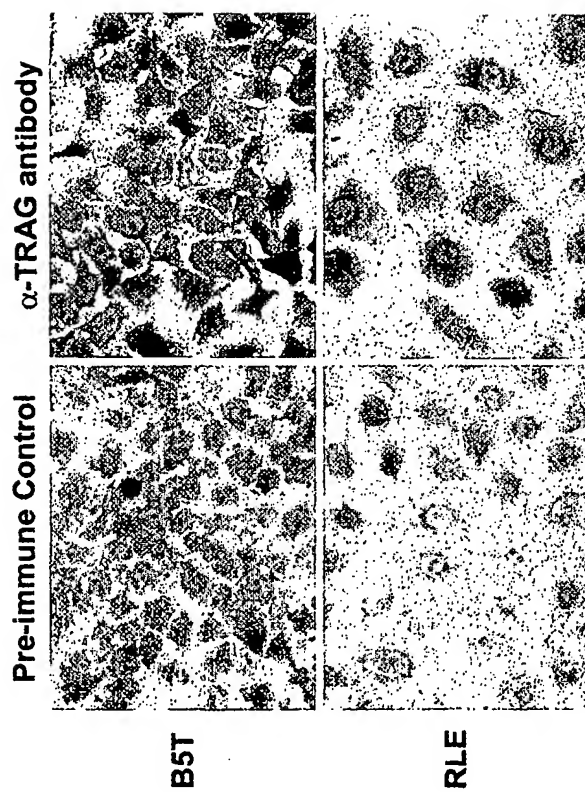


FIG. 6B



INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 01/04475

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12N15/12 C07K14/47 C12N5/10 C12N15/62 C07K16/18

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C07K C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, STRAND, BIOSIS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	SANDERS SEAN ET AL: "TRAG: A novel gene associated with TGF-beta resistance." PROCEEDINGS OF THE AMERICAN ASSOCIATION FOR CANCER RESEARCH ANNUAL, no. 41, March 2000 (2000-03), page 357 XP001011479 91st Annual Meeting of the American Association for Cancer Research.; San Francisco, California, USA; April 01-05, 2000, March, 2000 ISSN: 0197-016X the whole document ----- -/-	1-4,7,8, 10-14

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

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Date of the actual completion of the international search

10 July 2001

Date of mailing of the international search report

23/07/2001

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Holtorf, S

INTERNATIONAL SEARCH REPORT

International Application No

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	SANDERS S ET AL: "Assignment of WDR7 (alias TRAG, TGF-beta resistance associated gene) to orthologous regions of human chromosome 18q21.1fwdarwq22 and mouse chromosome 18D.1-E.3 by fluorescence in situ hybridization." CYTOGENETICS AND CELL GENETICS, vol. 88, no. 3-4, 2000, pages 324-325, XP001011475 Fourth International Chromosome 6 Workshop; England, Cambridge, UK; June 10-12, 1999 ISSN: 0301-0171 the whole document	1-4,7,8, 10-14
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X	& DATABASE EMBL SEQUENCE LIBRARY 'Online! 10 April 1998 (1998-04-10) OHARA, O., ET AL.: "Homo sapiens mRNA for KIAA0541 protein" cited in the application accession no. AB011113	1-4,7,8, 11-14
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A	DATTA PRAN K ET AL: "Identification of STRAP, a novel WD domain protein in transforming growth factor-beta signaling." JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 273, no. 52, 25 December 1998 (1998-12-25), pages 34671-34674, XP002171570 ISSN: 0021-9258 cited in the application	

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INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 01/04475

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	CHEN R -H ET AL: "A WD-DOMAIN PROTEIN THAT IS ASSOCIATED WITH AND PHOSPHORYLATED BY THE TYPE II TGF-BETA RECEPTOR" NATURE,GB,MACMILLAN JOURNALS LTD. LONDON, vol. 377, 12 October 1995 (1995-10-12), pages 548-552, XP002071531 ISSN: 0028-0836 cited in the application	
A	WO 99 43811 A (THORGEIRSSON SNORRI S ;US HEALTH (US); ZHANG MINGHUANG (US); WOITA) 2 September 1999 (1999-09-02) the whole document	
A	NEER E ET AL: "The ancient regulatory-protein family of WD-repeat proteins" NATURE,GB,MACMILLAN JOURNALS LTD. LONDON, vol. 371, 22 September 1994 (1994-09-22), pages 297-300, XP002081318 ISSN: 0028-0836 cited in the application	
P,X	DATABASE EMBL SEQUENCE LIBRARY 'Online! 11 November 2000 (2000-11-11) SANDERS, S. AND THORGEIRSSON, S.S.: "TAG: a novel gene associated with TGF-beta resistance" XP002171572 accession no. AF305813	1-4,7,8, 11-14

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Information on patent family members

International Application No
PCT/US 01/04475

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WO 9943811 A	02-09-1999	AU 2790599 A	15-09-1999